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OM protein - protein search, using sw model

Run on: June 2, 2004, 10:44:19 ; Search time 23 Seconds
(without alignments)
558,907 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKRVLAVCPAALFSSQALA.....PAFQQQLQKAKAFQHKK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A COMB.psp.*

2: /cgn2_6/ptodata/2/iaa/5B COMB.psp.*

3: /cgn2_6/ptodata/2/iaa/6A COMB.psp.*

4: /cgn2_6/ptodata/2/iaa/6B COMB.psp.*

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6: /cgn2_6/ptodata/2/iaa/backfiles1.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1276	100.0	249	3	US-08-750-145A-10
2	1276	100.0	249	3	US-08-975-698A-7
3	1276	100.0	249	3	US-09-417-090-4
4	1276	100.0	249	4	US-09-727-578-7
5	1190	93.3	231	3	US-08-750-145A-10
6	1190	93.3	231	3	US-08-975-698A-7
7	1190	93.3	231	3	US-09-417-090-8
8	1190	93.3	231	3	US-09-727-578-8
9	1158	90.8	248	3	US-08-750-145A-20
10	1158	90.8	248	3	US-08-975-698A-24
11	1158	90.8	248	3	US-09-417-090-24
12	1158	90.8	248	4	US-09-727-578-24
13	1155	90.5	253	4	US-09-489-039A-7933
14	1143	89.6	248	3	US-08-750-145A-22
15	1143	89.6	248	3	US-08-975-698A-26
16	1143	89.6	248	4	US-09-417-090-26
17	1143	89.6	248	4	US-09-727-578-26
18	1014	79.5	249	3	US-08-750-145A-3
19	1014	79.5	249	3	US-08-975-698A-3
20	1014	79.5	249	3	US-09-417-090-3
21	1014	79.5	249	4	US-09-727-578-3
22	1013	79.4	248	3	US-08-750-145A-18
23	1013	79.4	248	3	US-08-975-698A-22
24	1013	79.4	248	3	US-09-417-090-22
25	1013	79.4	248	4	US-09-727-578-22
26	962	75.4	229	3	US-08-750-145A-4
27	962	75.4	229	3	US-08-975-698A-4

28 962 75.4 229 3 US-09-417-090-4
29 962 75.4 229 4 US-09-727-578-4
30 780 61.1 244 3 US-08-750-145A-24
31 780 61.1 244 3 US-08-975-698A-28
32 780 61.1 244 3 US-09-417-090-28
33 780 61.1 244 4 US-09-727-578-28
34 314.5 24.6 252 1 US-07-717-332D-2
35 191 15.0 428 4 US-09-489-039A-10941
36 188.5 14.8 943 4 US-09-540-236-3458
37 175.5 13.8 253 4 US-09-252-991A-28557
38 152 11.9 987 4 US-09-543-681A-7785
39 96 7.5 824 4 US-09-711-164-377
40 90.5 7.1 244 4 US-09-252-991A-21937
41 89.5 7.0 244 4 US-09-543-681A-4595
42 85.5 6.7 187 4 US-09-328-352-7918
43 85.5 6.7 816 4 US-09-540-236-3443
44 84.5 6.6 337 4 US-09-328-352-6980
45 84 6.6 278 3 US-08-961-083-94

ALIGNMENTS

RESULT 1

US-08-750-145A-10

; Sequence 10, Application US/08750145A

; Patent No. 6010851

; GENERAL INFORMATION:

; APPLICANT: MIHARA, Yasuhiro

; APPLICANT: UTAGAWA, Takashi

; APPLICANT: YAMADA, Hideaki

; APPLICANT: ASANO, Yasuhisa

; TITLE OF INVENTION: Method for Producing Nucleoside-5'-

; TITLE OF INVENTION: Phosphate Ester

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.

; STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/750,145A

; FILING DATE: 01-JAN-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 7-149781

; FILING DATE: 05-May-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 8-094680

; FILING DATE: 26-Mar-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: NORMAN F. OBLON

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 249 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Escherichia blattae

; STRAIN: JCM 1650

US-08-975-698A-10
Query Match 100.0%; Score 1276; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-138;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKRVAVCFPAALFSSQALALVATGNTTTKPDLYLKNSEAINSLALPPPPAVGSIAP 60
Db 1 MKKRVAVCFPAALFSSQALALVATGNTTTKPDLYLKNSEAINSLALPPPPAVGSIAP 60
QY 61 LNDQAMVEQGLLNTERTGKLAADANLSSGCVANAFSGAFSPITEKDAPALHKLITNM 120
Db 61 LNDQAMVEQGLLNTERTGKLAADANLSSGCVANAFSGAFSPITEKDAPALHKLITNM 120
QY 121 IEDAGDLATRSKADHYRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
Db 121 IEDAGDLATRSKADHYRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
QY 181 EINFORQNEILKRGYELGQSRVICGYHWCSDVDAARVVGSAVVATHTNPAPQOOLQKAK 240
Db 181 EINFORQNEILKRGYELGQSRVICGYHWCSDVDAARVVGSAVVATHTNPAPQOOLQKAK 240
QY 241 AEFQHQKK 249
Db 241 AEFQHQKK 249

RESULT 2
US-08-975-698A-7
; Sequence 7, Application US/08975698A
; Patent No. 6015697
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,698A
; FILING DATE: 21-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
US-08-975-698A-7

Query Match 100.0%; Score 1276; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-138;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKKRVAVCFPAALFSSQALALVATGNTTTKPDLYLKNSEAINSLALPPPPAVGSIAP 60
Db 1 MKKRVAVCFPAALFSSQALALVATGNTTTKPDLYLKNSEAINSLALPPPPAVGSIAP 60
QY 61 LNDQAMVEQGLLNTERTGKLAADANLSSGCVANAFSGAFSPITEKDAPALHKLITNM 120
Db 61 LNDQAMVEQGLLNTERTGKLAADANLSSGCVANAFSGAFSPITEKDAPALHKLITNM 120
QY 121 IEDAGDLATRSKADHYRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
Db 121 IEDAGDLATRSKADHYRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
QY 181 EINFORQNEILKRGYELGQSRVICGYHWCSDVDAARVVGSAVVATHTNPAPQOOLQKAK 240
Db 181 EINFORQNEILKRGYELGQSRVICGYHWCSDVDAARVVGSAVVATHTNPAPQOOLQKAK 240
QY 241 AEFQHQKK 249
Db 241 AEFQHQKK 249
RESULT 3
US-09-417-090-7
; Sequence 7, Application US/09417090
; Patent No. 6207435
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,090
; FILING DATE: 13-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE: 21-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-417-090-7

Query Match 100.0%; Score 1276; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-138; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKVLAVCFALFSSQALALVATGNDTTTKPDLYLKNSSEINSLALLPPPPAVGSIAP 60
DB 1 MKKVLAVCFALFSSQALALVATGNDTTTKPDLYLKNSSEINSLALLPPPPAVGSIAP 60
QY 61 LNDQAMYEQGRLLRNTREGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
DB 61 LNDQAMYEQGRLLRNTREGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
QY 121 IEDAGLATRSADKDHMYRIRPFYGVSTCNTTEODKLSKNGSYSGHTSIGWATLVLA 180
DB 121 IEDAGLATRSADKDHMYRIRPFYGVSTCNTTEODKLSKNGSYSGHTSIGWATLVLA 180
QY 181 EINPQRQNEILKRGVELGQSRVICGHHQSDVDAAARVVGSAVVATLHTNPAFQQOLQKAK 240
DB 181 EINPQRQNEILKRGVELGQSRVICGHHQSDVDAAARVVGSAVVATLHTNPAFQQOLQKAK 240
QY 241 AEFAHQKK 249
DB 241 AEFAHQKK 249

RESULT 4

US-09-417-090-7
Sequence 7, Application US/09727578
Patent No. 635472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDRAXI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0895-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae

STRAIN: JCM 1650
US-09-727-578-7

Query Match 100.0%; Score 1276; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-138; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKVLAVCFALFSSQALALVATGNDTTTKPDLYLKNSSEINSLALLPPPPAVGSIAP 60
DB 1 MKKVLAVCFALFSSQALALVATGNDTTTKPDLYLKNSSEINSLALLPPPPAVGSIAP 60
QY 61 LNDQAMYEQGRLLRNTREGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
DB 61 LNDQAMYEQGRLLRNTREGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
QY 121 IEDAGLATRSADKDHMYRIRPFYGVSTCNTTEODKLSKNGSYSGHTSIGWATLVLA 180
DB 121 IEDAGLATRSADKDHMYRIRPFYGVSTCNTTEODKLSKNGSYSGHTSIGWATLVLA 180
QY 181 EINPQRQNEILKRGVELGQSRVICGHHQSDVDAAARVVGSAVVATLHTNPAFQQOLQKAK 240
DB 181 EINPQRQNEILKRGVELGQSRVICGHHQSDVDAAARVVGSAVVATLHTNPAFQQOLQKAK 240
QY 241 AEFAHQKK 249
DB 241 AEFAHQKK 249

RESULT 5

US-08-750-145A-11
Sequence 11, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
TITLE OF INVENTION: Phosphate Ester
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; US-08-750-145A-11

Query Match          93.3%  Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAYGSAFLNDQAMYEQGRLINRTER 78
Db 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAYGSAFLNDQAMYEQGRLINRTER 60
QY 79 GKLAEDANLSSGGVANAFSGAGSPITEKDAPALHKLLTNMIEDAGDLATRSKADHYMR 138
Db 61 GKLAEDANLSSGGVANAFSGAGSPITEKDAPALHKLLTNMIEDAGDLATRSKADHYMR 120
QY 139 IRPFAPFVGSTCNTTEODKLSKNGSYSGHTSIGWATALVLAELNPNQNEILKRGYELG 198
Db 121 IRPFAPFVGSTCNTTEODKLSKNGSYSGHTSIGWATALVLAELNPNQNEILKRGYELG 180
QY 199 QSRVICGYHQSDVDAAARVVGSAVAVATLHNPAPFQQQLQAKAEFAHQKK 249
Db 181 QSRVICGYHQSDVDAAARVVGSAVAVATLHNPAPFQQQLQAKAEFAHQKK 231

RESULT 6
US-08-975-698A-8
; Sequence 8, Application US/8975698A
; Patent No. 6015697
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,698A
; FILING DATE: 21-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; US-08-975-698A-8
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Query Match          93.3%  Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAYGSAFLNDQAMYEQGRLINRTER 78
Db 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAYGSAFLNDQAMYEQGRLINRTER 60
QY 79 GKLAEDANLSSGGVANAFSGAGSPITEKDAPALHKLLTNMIEDAGDLATRSKADHYMR 138
Db 61 GKLAEDANLSSGGVANAFSGAGSPITEKDAPALHKLLTNMIEDAGDLATRSKADHYMR 120
QY 139 IRPFAPFVGSTCNTTEODKLSKNGSYSGHTSIGWATALVLAELNPNQNEILKRGYELG 198
Db 121 IRPFAPFVGSTCNTTEODKLSKNGSYSGHTSIGWATALVLAELNPNQNEILKRGYELG 180
QY 199 QSRVICGYHQSDVDAAARVVGSAVAVATLHNPAPFQQQLQAKAEFAHQKK 249
Db 181 QSRVICGYHQSDVDAAARVVGSAVAVATLHNPAPFQQQLQAKAEFAHQKK 231

RESULT 7
US-09-417-090-8
; Sequence 8, Application US/09417090
; Patent No. 6207435
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,090
; FILING DATE: 13-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE: 21-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-417-090-8

Query Match          93.3%  Score 1190; DB 3; Length 231;
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Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 LALVATGNDTTTKPLLYLKNSAINSALLPPPAVGSIAFLNDQAMYEQGRLLRNT 78
1 LALVATGNDTTTKPLLYLKNSAINSALLPPPAVGSIAFLNDQAMYEQGRLLRNT 60
79 GKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNNIEDAGDLATRSKDHYMR 138
61 GKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNNIEDAGDLATRSKDHYMR 120
139 IRPFAPYGVSTNTTEQDKLKNKSYPSGHTSIGWATLVLAELNFORQNEILKRGYELG 198
121 IRPFAPYGVSTNTTEQDKLKNKSYPSGHTSIGWATLVLAELNFORQNEILKRGYELG 180
199 QSRVICGHWQSDVDAAARVGVSAVATLTNPAFQOOLQKAKAEFAHQKK 249
181 QSRVICGHWQSDVDAAARVGVSAVATLTNPAFQOOLQKAKAEFAHQKK 231

RESULT 8
US-09-727-578-8
; Sequence 8, Application US/09727578
; Patent No. 6355472
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
US-09-727-578-8

Query Match 93.3%; Score 1190; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 LALVATGNDTTTKPLLYLKNSAINSALLPPPAVGSIAFLNDQAMYEQGRLLRNT 78
1 LALVATGNDTTTKPLLYLKNSAINSALLPPPAVGSIAFLNDQAMYEQGRLLRNT 60
79 GKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNNIEDAGDLATRSKDHYMR 138
61 GKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNNIEDAGDLATRSKDHYMR 120
139 IRPFAPYGVSTNTTEQDKLKNKSYPSGHTSIGWATLVLAELNFORQNEILKRGYELG 198
121 IRPFAPYGVSTNTTEQDKLKNKSYPSGHTSIGWATLVLAELNFORQNEILKRGYELG 180
199 QSRVICGHWQSDVDAAARVGVSAVATLTNPAFQOOLQKAKAEFAHQKK 249
181 QSRVICGHWQSDVDAAARVGVSAVATLTNPAFQOOLQKAKAEFAHQKK 231

RESULT 9
US-08-750-145A-20
; Sequence 20, Application US/08750145A
; Patent No. 6010851
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: UTAGAWA, Takashi
; APPLICANT: YAMADA, Hideaki
; APPLICANT: ASANO, Yasuhisa
; TITLE OF INVENTION: Method for Producing Nucleoside-5'-
; TITLE OF INVENTION: Phosphate Ester
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08750,145A
; FILING DATE: 01-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-149781
; FILING DATE: 05-May-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-094680
; FILING DATE: 26-Mar-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: NORMAN F. OBLON
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Enterobacter aerogenes
; STRAIN: IFO 12010
US-08-750-145A-20

Query Match 90.8%; Score 1158; DB 3; Length 248;
Best Local Similarity 90.3%; Pred. No. 5.5e-125;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLAVCAALFSSQALVALVATGNDTTKPDLYLKNSEAINSLALLPPPEVGSIAF 60
DB 1 MKKRVLALCLASFVSNFAFVAGNDATTTPDLYLKNQAQIDSLALLPPPEVGSIAF 60
QY 61 INQAMVEQGRLLRNTERGKLAEDANLSSGVANAFSGAFSPITEKDAFALHKLITNM 120
DB 61 INQAMVEKGRLLRNTERGKLAEDANLSSGVANAFSSAFSPITEKDAFQJHKLITNM 120
QY 121 IEDAGDLATSAKHVNRIRPFAPYGVSTCNTTTEQDKLSKNGSVPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATSAKEKVMRIRPFAPYGVSTCNTTTEQDKLSKNGSVPSGHTSIGWATLVLA 180
QY 181 EIPQONEILKRGYELGOSRVICGHWQSDVDAARVGSVAVVATLHTNPAFQOOLQKAK 240
DB 181 EIPQONEILKRGYELGESRVICGHWQSDVDAARVGSVAVVATLHTNPAFQOOLQKAK 240
QY 241 AEPAQHOK 248
DB 241 DEFATQK 248

RESULT 10

US-08-975-698A-24
; Sequence 24, Application US/08975698A
; Patent No. 6315697
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,698A
; FILING DATE: 21-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Enterobacter aerogenes
; STRAIN: IFO 12010
; US-08-975-698A-24

Query Match 90.8%; Score 1158; DB 3; Length 248;
Best Local Similarity 90.3%; Pred. No. 5.5e-125;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLAVCAALFSSQALVALVATGNDTTKPDLYLKNSEAINSLALLPPPEVGSIAF 60
DB 1 MKKRVLALCLASFVSNFAFVAGNDATTTPDLYLKNQAQIDSLALLPPPEVGSIAF 60

DB 1 MKKRVLALCLASFVSNFAFVAGNDATTTPDLYLKNQAQIDSLALLPPPEVGSIAF 60
QY 61 INQAMVEQGRLLRNTERGKLAEDANLSSGVANAFSGAFSPITEKDAFALHKLITNM 120
DB 61 INQAMVEKGRLLRNTERGKLAEDANLSSGVANAFSSAFSPITEKDAFQJHKLITNM 120
QY 121 IEDAGDLATSAKHVNRIRPFAPYGVSTCNTTTEQDKLSKNGSVPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATSAKEKVMRIRPFAPYGVSTCNTTTEQDKLSKNGSVPSGHTSIGWATLVLA 180
QY 181 EIPQONEILKRGYELGOSRVICGHWQSDVDAARVGSVAVVATLHTNPAFQOOLQKAK 240
DB 181 EIPQONEILKRGYELGESRVICGHWQSDVDAARVGSVAVVATLHTNPAFQOOLQKAK 240
QY 241 AEPAQHOK 248
DB 241 DEFATQK 248

RESULT 11

US-09-417-090-24
; Sequence 24, Application US/09417090
; Patent No. 6207435
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,090
; FILING DATE: 13-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE: 21-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Enterobacter aerogenes
; STRAIN: IFO 12010
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
; US-09-417-090-24

Query Match 90.8%; Score 1158; DB 3; Length 248;
Best Local Similarity 90.3%; Pred. No. 5.5e-125;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
DB 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
QY 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSGPITKDPALHKLITNM 120
DB 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSGPITKDPALHKLITNM 120
QY 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLA 180
QY 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
DB 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
QY 241 AEFQHQK 248
DB 241 DEFQHQK 248

RESULT 12

US-09-727-578-24
; Sequence 24, Application US/09727578
; Patent No. 6355472
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Enterobacter aerogenes
; STRAIN: IFO 12010
US-09-727-578-24

Query Match 90.8%; Score 1158; DB 4; Length 248;
Best Local Similarity 90.3%; Pred. No. 5.5e-125;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
DB 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
QY 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSGPITKDPALHKLITNM 120
DB 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSGPITKDPALHKLITNM 120
QY 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLA 180
QY 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
DB 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
QY 241 AEFQHQK 248
DB 241 DEFQHQK 248

RESULT 13

US-09-489-039A-7933
; Sequence 7933, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7933
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7933

Query Match 90.5%; Score 1155; DB 4; Length 253;
Best Local Similarity 89.9%; Pred. No. 1.2e-124;
Matches 223; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
DB 6 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 65
QY 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSGPITKDPALHKLITNM 120
DB 66 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSGPITKDPALHKLITNM 125
QY 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLA 180
DB 126 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLA 185
QY 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
DB 186 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 245
QY 241 AEFQHQK 248
DB 246 DEFQHQK 253

RESULT 14

US-08-750-145A-22
; Sequence 22, Application US/08750145A
; Patent No. 6010851
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro

APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
TITLE OF INVENTION: Phosphate Ester
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-09468C
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: KORNAN F. OBLON

REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-750-145A-22

Query Match 89.6%; Score 1143; DB 3; Length 248;
Best Local Similarity 89.1%; Pred. No. 2.9e-123;
Matches 221; Conservative 15; Mismatches 115; Indels 0; Gaps 0;
Qy 1 MKKRVAVCFPAALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPVGSIAF 60
Db 1 MKKRVAVCFPAALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPVGSIAF 60
Qy 61 LNDQAMTEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHKLITNM 120
Db 61 LNDQAMTEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHKLITNM 120
Qy 121 IEDAGDLATRSADHYMRIRPFYFVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVIA 180
Db 121 IEDAGDLATRSADHYMRIRPFYFVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVIA 180
Qy 181 EINPQRONEILKRGYELGSRVICYGHWQSDVDAAIRVGSAAVATLTNPFAQQOQAK 240
Db 181 EINPQRONEILKRGYELGSRVICYGHWQSDVDAAIRVGSAAVATLTNPFAQQOQAK 240
Qy 241 AEPAQHOK 248
Db 241 DEFAQOK 248

RESULT 15
US-08-975-698A-26

Sequence 26, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-975-698A-26

Query Match 89.6%; Score 1143; DB 3; Length 248;
Best Local Similarity 89.1%; Pred. No. 2.9e-123;
Matches 221; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
Qy 1 MKKRVAVCFPAALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPVGSIAF 60
Db 1 MKKRVAVCFPAALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPVGSIAF 60
Qy 61 LNDQAMTEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHKLITNM 120
Db 61 LNDQAMTEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHKLITNM 120
Qy 121 IEDAGDLATRSADHYMRIRPFYFVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVIA 180
Db 121 IEDAGDLATRSADHYMRIRPFYFVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVIA 180
Qy 181 EINPQRONEILKRGYELGSRVICYGHWQSDVDAAIRVGSAAVATLTNPFAQQOQAK 240
Db 181 EINPQRONEILKRGYELGSRVICYGHWQSDVDAAIRVGSAAVATLTNPFAQQOQAK 240
Qy 241 AEPAQHOK 248
Db 241 DEFAQOK 248

Search completed: June 2, 2004, 10:48:05
Job time : 24 secs

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OX protein - protein search, using sw model

Run on: June 2, 2004, 10:47:04 ; Search time 49 Seconds
(without alignments)
1429.660 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKKRVLAFCFAALFSSQALA.....PAFOOQLQKAKAFQK 249

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubpaa/ECTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	143	11.2	622	9	US-09-738-626-4817
2	93.5	7.8	353	15	US-10-374-780A-1704
3	97.5	7.6	1610	15	US-10-369-493-3448
4	96.5	7.6	305	15	US-10-369-493-3179
5	96	7.5	178	12	US-10-282-122A-77490
6	96	7.5	824	12	US-10-282-122A-42600
7	95	7.5	824	14	US-10-287-274-377
8	94.5	7.4	515	16	US-10-389-566-351
9	93.5	7.3	704	14	US-10-213-990-21
10	93	7.3	608	15	US-10-369-493-5228
11	92.5	7.2	159	9	US-09-738-626-6679
12	92.5	7.2	159	12	US-10-627-476-102
13	91	7.1	201	14	US-10-156-761-7677
14	90.5	7.1	437	12	US-10-282-122A-66585
15	89	7.0	497	12	US-10-424-599-159028

16	88.5	6.9	168	9	US-09-738-626-6676
17	88	6.9	921	14	US-10-281-866-2
18	87	6.8	408	15	US-10-369-493-9754
19	86	6.7	273	12	US-10-425-114-63365
20	86	6.7	665	12	US-10-282-122A-51723
21	86	6.7	1573	14	US-10-214-766-35
22	85.5	6.7	221	12	US-10-282-122A-69103
23	85.5	6.7	774	12	US-10-282-122A-63166
24	85	6.7	766	14	US-10-317-832-120
25	84.5	6.6	4317	12	US-10-282-122A-67862
26	84	6.6	278	9	US-09-765-272-94
27	84	6.6	571	9	US-09-765-272-4
28	84	6.6	981	14	US-10-156-761-15071
29	83.5	6.5	260	16	US-10-408-765A-1756
30	83	6.5	268	12	US-10-282-122A-63138
31	83	6.5	378	15	US-10-369-493-5080
32	83	6.5	535	14	US-10-032-201B-232
33	82.5	6.5	402	14	US-10-081-051-16
34	82	6.4	610	12	US-10-282-122A-45687
35	81.5	6.4	198	12	US-10-282-122A-50258
36	81.5	6.4	265	12	US-10-424-599-243256
37	81.5	6.4	349	15	US-10-150-048-4
38	81.5	6.4	518	9	US-09-738-626-4323
39	81.5	6.4	928	15	US-10-379-632-33
40	81.5	6.4	1063	15	US-10-379-632-84
41	81.5	6.4	1089	15	US-10-379-632-109
42	81.5	6.4	1113	15	US-10-379-632-103
43	81.5	6.4	1209	15	US-10-379-632-96
44	81	6.3	298	12	US-10-282-122A-47486
45	81	6.3	490	15	US-10-369-493-2735

ALIGNMENTS

RESULT 1

US-09-738-626-4817

; Sequence 4817, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI

; APPLICANT: MIZOGUCHI, HIROSHI

; APPLICANT: ANDO, SEIKO

; APPLICANT: HAYASHI, MIKIRO

; APPLICANT: OCHIAI, KEIKO

; APPLICANT: YOKOI, HARUHIKO

; APPLICANT: TATEISHI, NAOKO

; APPLICANT: SENOH, AKIHIRO

; APPLICANT: IKEDA, MASATO

; APPLICANT: OZAKI, AKIO

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-125

; CURRENT APPLICATION NUMBER: US/09/738,626

; CURRENT FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: JP 99/377484

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: JP 00/159162

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: JP 00/280988

; PRIOR FILING DATE: 2000-08-03

; NUMBER OF SEQ ID NOS: 7059

; SOFTWARE: Patent in ver. 3.0

; SEQ ID NO 4817

; LENGTH: 622

; TYPES: PRT

; ORGANISM: Corynebacterium glutamicum

US-09-738-626-4817

Query Match 11.2%; Score 143; DB 9; Length 622;

Best Local Similarity 27.4%; Pred. No. 3.3e-06;

Matches 49; Conservative 24; Mismatches 72; Indels 34; Gaps 6;

QY 83 AEDANLSSGGVANA----FSGAFGSPITEKADALHKLTLNIEDAGLATSADHYMR 138

Db 159 ATTVKYNDGNGVNGWAETGELGSLVDLIEAIRQHAATSN-----NAKAYQY 207
QY 139 IRFPAP-----YGVST---CNTTEQD--KLSKNGSVPSGHTSIGWATALVLAEIN 183
Db 208 PRFYRWTESIEPEAWGSGVDMPEYANPLRKDESEASADGGPPSGHTSAGGMAITGLAYAF 267
QY 184 EPCNCELKRGVELGQSEVLCGVHMQSDVDAARVVGSAVVATLHTNPAFCQQLQKAKAE 242
Db 268 PQDYKLLMTAAELGESRIQLGMSPLDVGGRVLSTAIRAGALNDP-----NLSVRAE 322

RESULT 2

US-10-374-780A-1704
; Sequence 1704, Application US/10374780A
; Publication No. US20040019927A1

GENERAL INFORMATION:

; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

; FILE REFERENCE: MEI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A

; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: 09/837,944

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/310,847

; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 09/934,455

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/336,049

; PRIOR FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/338,692

; PRIOR FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: 10/171,468

; PRIOR FILING DATE: 2002-06-14

; PRIOR APPLICATION NUMBER: 10/225,066

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 10/225,067

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 10/225,068

; PRIOR FILING DATE: 2002-08-09

; NUMBER OF SEQ ID NOS: 2906

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1704

; LENGTH: 353

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Orthologous to G1652

US-10-374-780A-1704

Query Match 7.8%; Score 99.5; DB 15; Length 353;

Best Local Similarity 24.5%; Pred. No. 0.077; 92; Indels 71; Gaps 13;

Matches 63; Conservative 31; Mismatches 31

QY 41 EAINSLALLP--PPPVGSIATLNDQMYEGRLRN---TERGKLAED-----AN 87
Db 13 ETLQHILPLATPPPPAGGYA--GENATFPQLALRESSVQNGMAPPEPTAHECHASN 70
QY 88 LSSGGVANAFSGAFSPITEKDA-----PALHKLITNMIED 123

Db 71 SWSSGDDTDSVSGGGGAVMEHDGHTSPNSVRCAGGGGGGGGGLWVPVSNFSSAMTQP 130
QY 124 AGDIATSAKDHYMRIRPFAPYG-----YSTNTTQDQKLSK--NSGYPGHTSI 171
Db 131 CNDQATPSNPPTTTTRAR-----YGGGVRYLPAAVSPSPSAQTRRASSKXGNGSGSSSA 186
QY 172 G-WATALVLAEINPQRCNEILLKRGVELGQSEVLCGVHMQSDVDAARVVGSAVVATLHTNP 230
Db 187 APYACEHIIAE--RKRREKINQRFIEL--SVIPEL---KXMDKATILSDAV----- 231
QY 231 AFQOQLOKAKAEFAHQ 247
Db 232 RYVKEMQEKLELEHQ 248

RESULT 3

US-10-369-493-3448

; Sequence 3448, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 3448

; LENGTH: 1610

; TYPE: PRT

; ORGANISM: Neurospora crassa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(1610)

; OTHER INFORMATION: unsure at all xaa locations

US-10-369-493-3448

Query Match 7.6%; Score 97.5; DB 15; Length 1610;

Best Local Similarity 26.4%; Pred. No. 1.3;

Matches 53; Conservative 21; Mismatches 70; Indels 57; Gaps 10;

QY 18 ALALVAT-GNDTTTKPDILYLNKSE-----AINSLALLPPPPAV-----GSIA-PL 61

Db 274 ALPLGATMGNDNTMTGNLDEAHGSEQHPPPPFASVNVDPDPGVIYEDPTAEACGKIQFEL 333

QY 62 ND-----QAMVEQGRLLRNTERKLAEDANLSSGGVANAFSGAFSGPITEKDA---PA 112

Db 334 NNLTTTLQTNKLRDMLKTHQW-----FASHLVEERAKKQPN 374

QY 113 LHKL---LITNMIEDAGDIATSAKDHYMRIRPFAPYGVSTCTMTTQDQKLSKNGSVPSGHT 169

Db 375 YHOVYLD-VKMFEDK-SLWAEVLRETVYVQRMENLSDVTLQNSTERTHLKNLG----- 426

QY 170 SIGNATALVLAEINPQRCNEI 190

Db 427 --GWLGLTLARNKPKIHRNI 445

RESULT 4

US-10-369-493-3179

; Sequence 3179, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xiaofeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-13(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3179
LENGTH: 305
TYPE: PRT
ORGANISM: Neurospora crassa
US-10-369-493-3179

Query Match 7.6%; Score 96.5; DB 15; Length 305;
Best Local Similarity 22.2%; Pred. No. 0.13;
Matches 43; Conservative 29; Mismatches 79; Indels 43; Gaps 7;
QY 3 KRVAVCFALFSSQALVALVATGNDTTTKEDLYLKNSEA:NSLALLPPPPAVGSIAPLN 62
DB 84 KRSIDACLAJ:-----DGHK-DIP-----EPARIDPKVPLESTLXLE 122
QY 63 DQ:-----AMYEQRLNTERGKLAEDANLS-----SGGVANAFSGAPGS 103
DB 123 DEVYSGIIGIGLSEVSAAITKAVKITKAAVEVEISLWATHLENGVAEA-CAEFGI 181
QY 104 PITEKAPALHKLITNMIEDAGLATSADKHMYRPPAFYGVSTCNTTQDKLSKNGS 163
DB 182 FLIAY-SPIGSGMLTGQIKTLDLADDFRRHFRFPENFH-LNIQLVSLNELAKKG 239
QY 164 YPSGHTSIGWATAL 177
DB 240 YTPAQLAINVKSL 253

RESULT 5
US-10-282-122A-77490
Sequence 77490, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42600
LENGTH: 824

PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 77490
LENGTH: 178
TYPE: PRT
ORGANISM: Vibrio cholerae
US-10-282-122A-77490

Query Match 7.5%; Score 96; DB 12; Length 178;
Best Local Similarity 31.0%; Pred. No. 0.066;
Matches 27; Conservative 14; Mismatches 42; Indels 4; Gaps 1;
QY 133 KDHMYRIRPFAYGVSTCNTTQDKLSKNGSYPSGHTSIGWATALVLAEINPORQNEILK 192
DB 81 KNSPQRRPQELSALVTAYITPDSRY----SLPSGHTAAAFVMTLIGYIYPHWYAVALC 136
QY 193 RGYELGQSRVICGVHWSQDNDAARVVG 219
DB 137 WAGLIGLARVLGVHLSVDVIAGALLG 163

RESULT 6
US-10-282-122A-42600
Sequence 42600, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42600
LENGTH: 824


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; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-21

Query Match      7.3%; Score 93.5; DB 14; Length 704;
Best Local Similarity 21.3%; Pred. No. 0.99;
Matches 53; Conservative 44; Mismatches 67; Indels 85; Gaps 14;

Qy 22 VATGNDTTTKPDLYLKNSKSEALNSLALPPPPAVGSIAPLNDQAWYEQGRLLNTERGK- 80
Db 151 ILLASPSQSNFDYYITWTRDAALTKYL-----VGSFADHDPAIQ---RIIEDYVESQA 202
Qy 81 ----LAEDANLSSGGV-----ANAFSGAFGSPITEKDPALHKL-----LTNMIEDA 124
Db 203 HLQIVSPNSGNLSSGGLGEPKLRVGSFAHSGWGRP--QSDGPAL3ATLLISYANLMDN 260
Qy 125 GDLATRSNAKHMYRIRP-----AFYGVSTCTNTEQDKLSKNGSPSGHTSIGHAT 175
Db 261 GYFSTVSS-----IWPLIQNDLSYLTEFWNSSTFDLME-----VGSSEF-----FTT 304
Qy 176 ALVLAEINPQRNEILKRGVELGO-----SRVIC--GYHWQSDVDAAARVVG 220
Db 305 AV-----QHQLARKGALLAQLGKTCNQCQSQAPQVLCFLQTY-----TGS 346
Qy 221 AVVATLHTN 229
Db 347 SILANLYSD 355

RESULT 10
US-10-369-493-5228
; Sequence 5228, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiaofeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5228
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5228

Query Match      7.3%; Score 93; DB 15; Length 608;
Best Local Similarity 23.5%; Pred. No. 0.9;
Matches 42; Conservative 19; Mismatches 78; Indels 40; Gaps 5;

Qy 84 EDANLSSGGVAVAFSGFSGP-TEKDPALHKLNTNMIEDAGDLATRSNAKHMYRIRPPA 143
Db 456 EDGQAFGGGGNGMNAFGMDV-ENDDPLALRVSMEEERARQAAAAAN-----505
Qy 144 FYGVSTCTNTEQDKLSKNGSPSGHTSIG-----WATLVLAELNIPQRNEILKRG 194
Db 506 --GGAADSGADAEEVAAAAAAPLEEMDNGAMTEEQLEWALRLSMQENAPAFQPVQV---559
Qy 195 YELGQSRVICGYHWQSDVDAAARVGSVAVVATHTNPAFCQ-----LQAKAEFAHQKK 249
Db 560 -----CHEQMDVGGAPAVGDNLDLANNPELLQIVVDLPAANAEKDDQKEK 607

RESULT 11
US-09-738-626-6679
; Sequence 6679, Application US/09738626
```

```
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patentin ver. 3.0
; SEQ ID NO 6679
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6679

Query Match      7.2%; Score 92.5; DB 9; Length 159;
Best Local Similarity 24.2%; Pred. No. 0.13;
Matches 40; Conservative 26; Mismatches 54; Indels 45; Gaps 8;

Qy 93 VANAFSG---AFGSPI---TEKDPAL---HKLNTNMIEDA-----GDLATESAK 133
Db 5 ILDAFGLRVTWLSPIILFTQTLTFVVALVWGLRKSGATAPVGLANLISHFLK 64
Qy 134 DHYMRIRPFAYGVSTCTNTEQDKLSKNGSPSGHTSIGWATLVLAELNIPQRNEILK 193
Db 55 RAPEPRP-----NTAEHLVVTETNFSFSGH-AVGAACAVAVGYS-----VNR 107
Qy 194 GYEL-----GQSRVICGYHWQSDVDAAARVGSVAVVATHTN 229
Db 108 WVKLTALVIALVGL-SRLVGVGVHWPSPDVLGAWGALGALTSTVVVFTS 152

RESULT 12
US-10-627-476-102
; Sequence 102, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CPCN
; CURRENT APPLICATION NUMBER: US/10/627,476
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
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; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 102
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-627-476-102

Query March 7.2%; Score 92.5; DB 12; Length 159;
Best Local Similarity 24.2%; Pred. No. 0.13;
Matches 40; Conservative 26; Mismatches 54; Indels 45; Gaps 8;

Qy 93 VANAFSG---AFSGPI---TEKDAPL---HKLITNIEDA-----GDLATRSK 133
Db 5 ILDAFGLRVTWLSPILETLTGPTILMFYALVWGLRKSATAPAVGLAKLISHFLK 64
Qy 134 DYMRIFFAFYGVSTCTNTEQDKLXNGSVPSGHTSIGWATALVLAELINPQNEILKR 193
Db 65 RAPERPRP-----NTAEHLVVENFSPFSGH-AVGAACAVAVGYS-----VNR 107
Qy 194 GYEL-----GQSRVICYHMQSDVDAAVVVGSVAVATLHN 229
Db 108 WKKLITLWVIALVGLSLRYGVHVPSPDLVAGWALGALTSVVWF'S 152

RESULT 13
US-10-156-761-7677
; Sequence 7677, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, HIROSHI
; APPLICANT: HORIKAWA, JUN
; APPLICANT: SHIBA, TADAYOSH
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, YASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7677
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7677

Query Match 7.1%; Score 91; DB 14; Length 201;
Best Local Similarity 30.3%; Pred. No. 0.28;
Matches 33; Conservative 11; Mismatches 45; Indels 20; Gaps 3;

Qy 142 FAFYGVG-----TCN-----TTEQDKLXNGSVPSGHTSIGWATALVLAELINPQ 185
Db 74 FAAYGVNDVLKLVREDRPPCOSLQVITLACAPGDSFPSPNSHTAIAAAAMALLFVSRR 133
Qy 186 RQNEILKRGVIGOSRVICGVHMQSDVDAAEFVGSVAVA---T-HTNP 230
Db 134 LGVAAGACAMAASRVVWGAHPHDVAAGVVVGVGVAALAMVTLRRQP 182
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```

RESULT 14
US-10-282-122A-66585
; Sequence 66585, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malore, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78514
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66585
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66585

Query Match 7.1%; Score 90.5; DB 12; Length 437;
Best Local Similarity 26.4%; Pred. No. 1;
Matches 34; Conservative 24; Mismatches 48; Indels 23; Gaps 5;

Qy 105 ITEKDAPALMKLITNIEDAGDLATRSKAKOHYMRIRPFAYGVSTCTNTEQDKLXNGSY 164
Db 274 LTRQWRPAIFAGT-LVGTA--LANQTLKTLFARARPEVL-----AEPLS-SFSF 319
Qy 165 PSHTSIGWATALVLAELINPQNEILKRGY-----ELGOSRVICGVHMQSDVDAA 215
Db 320 PSGHSSASFAFFLTGLVLAASRQPPRWRLTWLLAVIPSLIALSRVLYGVHWPFSDIVAG 379
Qy 216 RVGSAVVA 224
Db 380 ALLATTVC 388

RESULT 15
US-10-424-599-159028
; Sequence 159028, Application US/10424599
; Publication No. US20040031072A1
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 10:43:19 ; Search time 20 Seconds
(without alignments)
1197.584 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKKRVLAFCFAALFSSQALA.....PAFQOOLQKAKFAHQKX 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014	79.5	249	1 S19187	acid phosphatase (
2	1013	79.4	248	1 PAOFCS	acid phosphatase (
3	486	38.1	250	1 A41330	acid phosphatase (
4	477	37.4	250	2 A1025	acid phosphatase (
5	339.5	26.6	264	1 A12044	acid phosphatase (
6	274.5	21.5	258	2 E87293	acid phosphatase (
7	189.5	14.9	2314	2 T28638	hypothetical prote
8	175.5	13.8	241	2 C83621	probable acid phos
9	167	13.1	591	2 C96991	uncharacterized pr
10	141	11.1	660	2 A83118	serine proteinase
11	141	11.1	660	2 E98169	serine proteinase
12	105	8.2	145	2 F75447	vanadium chlorop
13	99.5	7.8	259	2 A87623	PAF2 homolog prote
14	96.5	7.6	256	2 G39845	dihydroxylate deh
15	96	7.5	178	2 D82070	conserved hypothet
16	96	7.5	824	2 D64738	ATP-dependent heli
17	95	7.4	320	2 A82020	hypothetical prote
18	94	7.4	824	2 H85498	helicase, ATP-depe
19	94	7.4	824	2 H90647	ATP-dependent heli
20	93	7.3	608	2 D87912	protein B0205.3 [i
21	91	7.1	217	2 D97672	hypothetical prote
22	91	7.1	242	2 A82897	conserved hypothet
23	90.5	7.1	437	2 H83143	hypothetical prote
24	89.5	7.0	1157	2 A35152	PAS1 protein - yea
25	88	6.9	589	2 T29897	hypothetical prote
26	86.5	6.8	368	2 A82148	probable porin vc1
27	86.5	6.8	649	2 S74823	N-acetylmuramoyl-L
28	86	6.7	292	2 A36647	phosphatidyglycer
29	86	6.7	665	2 F97032	beta-glucosidase i

vacb-like (shigell
3-dehydroquinat s
probable adhesin Z
probable adhesin E
2-C-methyl-D-eryth
P element transpos
gene posterior sex
dtdp-4-dehydroham
mannose-1-phosphat
immunoglobulin A1
pyridoxine biosynt
conserved hypothet
hypothetical prote
asparagine synthet
probable thioedox
probable integrase

ALIGNMENTS

RESULT 1

S19187
acid phosphatase (EC 3.1.3.2) - Morganella morganii
C:Species: Morganella morganii
C>Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 18-Aug-2003
C:Accession: S19187
R:Thaller, M.C.; Berlutti, F.; Schippa, S.; Rosolini, G.M.
submitted to the EMBL Data Library, February 1992
A:Description: Sequencing the Morganella morganii phoC gene coding for a periplasmic ac
A:Reference number: S19187
A:Accession: S19187
A:Molecule type: DNA
A:Residues: 1-249 <THA>
A:Cross-references: EMBL:X64444; NID:G44463; PIDN:CAA45774.1; PID:G44464
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoester hydrolase
F:109-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 79.5%; Score 1014; DB 1; Length 249;
Best Local Similarity 77.1%; Pred. No. 2.5e-81;
Matches 192; Conservative 23; Mismatches 34; Indels 0; Gaps 0;

QY	1	MKKRVLAFCFAALFSSQALALVATNDTTKEDLYLKNSEAINSLALPPEAVGSIAF	60
DB	1	MKKNTIACLSFLSLSALAAIPAGNDATTKEDLYLKNQQAIDSLKLEPPPEVGSIOF	60
QY	61	LNDAQMYEQGRLLRNTERGKLAEDANLSSGGVANAFSGAFSGPITEKDAFALHKLITNM	120
DB	61	LNDAQMYEKGRLRNTERGKQAQADADLAAGGVATAFSGAFGYPITEKDSPELYKLLTNM	120
QY	121	IEDAGDLATRSADKHYMRIRPFYGVSTNTTEQDKLSKNGSPSGHTSIGWATLVLA	180
DB	121	IEDAGDLATRSADKHYMRIRPFYGVSTNTTEQDKLSKNGSPSGHTSIGWATLVLA	180
QY	181	EINPORQNEILKRGVELQSGVICGHWQSDVDAARVGVSAVATLHTNPAPQOOLQAK	240
DB	181	EVPANQDAIILRGYQLGQSRVICGHWQSDVDAARVGVSAVATLHTNPAPQOOLQAK	240
QY	241	AEFAQHOKX 249	
DB	241	QEFAKSKX 249	

RESULT 2

PAOFCS
acid phosphatase (EC 3.1.3.2) - Providencia stuartii
C:Species: Providencia stuartii
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Aug-2003
C:Accession: S19888
R:Riccio, M.L.; Lombardi, G.; Chiesurin, A.; Satta, G.
submitted to the EMBL Data Library, February 1992
A:Reference number: S19888

A:Accession: S19888
A:Molecule type: DNA
A:Residues: 1-248 <RIC>
A:Cross-references: EMBL:X64820; NID:G45861; PIDN:CAA46032.1; PID:G45862
C:Genetics:
C:Gene: phoN
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoester hydrolase
F:109-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 79.4%; Score 1013; DB 1; Length 248;
Best Local Similarity 77.4%; Pred. No. 3e-81;
Matches 192; Conservative 26; Mismatches 30; Indels 0; Gaps 0;

QY 1 MKKRVAVCFNAALFSSQALVALVATGNTTTKPDLYLKNSEAFNSIALLPRAVGSIAF 60
DB 1 MKKLLAVFCAGAFVSTSVFAAPGNDVTTKPDLYLKNQADSLALLPPPEVGSILF 60

QY 61 LNDQAMVEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSPITTEKDAPEIHKLLTNM 120
DB 61 LNDQAMVEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSPITTEKDAPEIHKLLTNM 120

QY 121 IEDAGLATRSKADHYNRIRPPAFYGVSTNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
DB 121 IEDAGLATRSKADHYNRIRPPAFYGVSTNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180

QY 181 EIPNPNQNEILKRGYELGQSRVIGYHWSQVDAARVVGSAVATLTNPAFQOOLQAK 240
DB 181 EIPNPNQNEILKRGYELGQSRVIGYHWSQVDAARVVGSAVATLTNPAFQOOLQAK 240

QY 241 AEPAQK 248
DB 241 DEFAKUK 248

RESULT 3
A41330
A:Accession: S20958
A:Molecule type: DNA
A:Residues: 1-250 <GRO>
A:Cross-references: EMBL:X63599; NID:G47823; PIDN:CAA45144.1; PID:G47824
R:Kasahara, M.; Nakata, A.; Shinagawa, H.
J. Bacteriol. 173, 6760-6765, 1991
A:Title: Molecular analysis of the Salmonella typhimurium phoN gene, which encodes nonse
A:Reference number: A41330; MUID:92041557; PMID:1938882
A:Accession: A41330
A:Molecule type: DNA
A:Residues: 1-229, 'SVRS' <KAS>
A:Cross-references: GB:X59036; NID:G48894; PIDN:CAA41760.1; PID:G48895
C:Genetics:
A:Gene: phoN
A:Map position: 96 min
A:Note: regulated by the two-component regulatory system consisting of phoP and phoQ
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: periplasmic space; phosphoric monoester hydrolase
F:108-221/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 38.1%; Score 486; DB 1; Length 250;
Best Local Similarity 43.0%; Pred. No. 4.6e-35;
Matches 104; Conservative 33; Mismatches 95; Indels 10; Gaps 2;

QY 1 MKKRVAVCFNAALFSSQALVALVATGNTTTKPDLYLKNSEAFNSIALLPRAVGSIAF 60
DB 1 MKSRYLVFFLLIVAKYTS-----ETVQF---FHSPEESVNSQFYLPPEPPGNDPPAY 50

QY 61 LNDQAMVEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSPITTEKDAPEIHKLLTNM 120
DB 51 RYDKAEYFKYAIKGSFRWKAEDADVSENIARIFSPVVGAKINFDPEETWNMLKUL 110

QY 121 IEDAGLATRSKADHYNRIRPPAFYGVSTNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
DB 111 LTMGGYVATASAKKYVMTPTFPVLEHNHSTCRPEDNLTNRKNGSYPSGHTYGTLLALVLS 170

QY 181 EIPNPNQNEILKRGYELGQSRVIGYHWSQVDAARVVGSAVATLTNPAFQOOLQAK 240
DB 171 EAPPEAQELARRWEGFQSRVIGCAHWQSDVDAGRYVGAVEFARLQTIPIAFQSLAKVR 230

QY 241 AE 242
DB 231 EE 232

RESULT 4
AF1025
A:Accession: AF1025
A:Molecule type: DNA
A:Residues: 1-250 <PAR>
A:Cross-references: GB:ALU513382; PIDN:CAD09303.1; PID:G16505305; GSPDB:GN00176
C:Genetics:
A:Gene: phoN
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic d
C:Keywords: phosphoric monoester hydrolase

Query Match 37.4%; Score 477; DB 2; Length 250;
Best Local Similarity 47.0%; Pred. No. 2.9e-34;
Matches 95; Conservative 31; Mismatches 75; Indels 0; Gaps 0;

QY 41 EAINSLALLPPPPAVGSTAFNDQAMVEQGRLLRNTERRGKLAEDANLSSGGVANAFSGA 100
DB 31 ESVNSQFYLPPEPPGNDPPAFRYDKAEYFKYAIKGSFRWKAEDADVSENIARIFSPV 90

QY 101 FGSPITEKDAPEIHKLLTNMIEDAGLATRSKADHYNRIRPPAFYGVSTNTTTEQDKLSK 160
DB 91 VGAKINFDPEETWNMLKULKMGYYATASAKKYVMTPTFPVLEHNHSTCRPEDNLTNRK 150

QY 161 NGSYPSGHTSIGWATALVLAIEINPQRQNEILKRGYELGQSRVIGYHWSQVDAARVVG 220
DB 151 DGSYPSGHTYGTLLALVLSQAPERAQELARRWEGFQSRVIGCAHWQSDVDAGRYVGA 210

QY 221 AVVATLTNPAFQOOLQAKAE 242
DB 211 VEFARLQTIPIAFQSLAKVR 232

RESULT 5
A32044
A:Accession: A32044
A:Molecule type: DNA
A:Residues: 1-231, 'SVRS' <ZYM>
A:Cross-references: GB:3.1.3.2 - Zymomonas mobilis
C:Species: Zymomonas mobilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2003
C:Accession: A32044
R:Pond, J.L.; Eddy, C.K.; Mackenzie, K.F.; Conway, T.; Borecky, D.J.; Ingram, L.O.
J. Bacteriol. 171, 767-774, 1989
A:Title: Cloning, sequencing, and characterization of the principal acid phosphatase, tl
A:Reference number: A32044; MUID:89123152; PMID:23914872

A;Accession: A32044

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-264 <PON>

A;Cross-references: GB:M24141; NID:gl55613; PIDN:AAA27700.1; PID:gl55614

C;Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

C;Keywords: phosphoric monoester hydrolase

F;99-212/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 26.6%; Score 339.5; DB 1; Length 264;

Best Local Similarity 33.6%; Pred. No. 3.4e-22;

Matches 80; Conservative 42; Mismatches 109; Indels 7; Gaps 3;

QY 8 VCPALFS----SOMALVATGNTTTKPDLYLKNSEAINSLALPPPPAVGSIAPLNDQ 64

DB 8 ICMIALTSGLVSLGQSVAHTKSEPSSTYHFSD---FLYLAPPPTSGSPLOAHDD 64

QY 65 AMVEQGLLRNTERGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNMIEDA 124

DB 65 QTENSTQLKSGTSWALATQADLHLASVLDYACAGWNIDIAQLPHANLIKRALTE 124

QY 125 GDATRSADHYMRIRPFPAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNP 184

DB 125 YDOJGR-AKNNWNRKRPVDTQDICTEKDREGLKQSGSYPSGHTTICMSVALILAEIP 183

QY 185 QRQNEIILKRGVELGQSRVILCGHYHCSDVDARVVGSAVVILHTNPATQOOLQAKAE 242

DB 184 DHAANILQGOIFGTSRIVCGAHWFSDVQAGYIMASGEIALHGDADPRDMELARKE 241

RESULT 6

E87293

acid phosphatase [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 25-Aug-2003

C;Accession: E87293

R;Niernan, M.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

n, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: E87293

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-258 <STO>

A;Cross-references: GB:AE005673; NID:gl3421511; PIDN:AAK22345.1; GSPDB:GN00148

C;Genetics:

A;Gene: CC0358

C;Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

Query Match

Best Local Similarity 21.5%; Score 274.5; DB 2; Length 258;

Matches 80; Conservative 35; Mismatches 109; Indels 7; Gaps 7;

QY 13 LFSSQALVALVATGNTTTKPDLYLKNSEAINSLALPPPPAVGSIAPLNDQAMVEQRL 72

DB 6 LVTTAALMLTGATLSGDAPSNRYLAKG-VFDARDHLPPPPAKGSEALRDREIFATRA 64

QY 73 LRNTERGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNMIEDAGLATRS 131

DB 65 LKOTPRSLAQED-NVER-KVLGDYACALGTPSPERN-PKLVATLLRMSRDRS-AVAG 120

QY 132 AKDHYMRIRPFPAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPQNEIL 191

DB 121 PKLYRRPRPFSEGPIC-IKRSIGLALSPDYPGSHATWGSVLVAEAPDRREAIL 179

QY 192 KRGVELGQSRVILCGHYHCSDVDARVVGSAVVILHTNPATQOOLQAKAE 242

DB 180 ARAQAYGESRVVCGVHNNSSVAGRMNAENILSALKSSDAFKADLAARAE 230

RESULT 7

T28698

Hypothetical protein - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T28698

R;Parkhill, J.; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, January 1999

A;Reference number: Z20512

A;Accession: T28698

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2314 <PAZ>

A;Cross-references: EMBL:AL023496; NID:el292348; PID:el292365; PIDN:CAA18915.1

Query Match 14.9%; Score 189.5; DB 2; Length 2314;

Best Local Similarity 29.0%; Pred. No. 8.5e-08;

Matches 56; Conservative 33; Mismatches 83; Indels 21; Gaps 7;

QY 61 LNDQAMVEQGLLRNTERGKL-AAEDANLS-SGGVANAFSGAFSPITEKDPALHKLIT 118

DB 1862 VNNAATQOO-----VDRAEVDASNTVTWADGLGSLGPLYGEALKEGRLPKTSALFS 1915

QY 119 NMIE--DAGDLATRSADHYMRIRPF---AFYGVSTCNTTEQDK----LSKNGSYPSGHT 169

DB 1916 RVNENLDTHD-----AAKNHYQVLRPYVRVLRGAGDGVAVESQSSVSLGAGQSGYPSGHT 1771

QY 170 SIGWATLVLAELNPQNEILKRGVELGQSRVILCGHYHCSDVDARVVGSAVVILHTN 229

DB 1972 YGGVEAGTILATLLPDLAPSIARTSEYGDNRIVLGFHYPLDVMGGRITPAQTVAHRWAD 2031

QY 230 PAFQOOLQAKAE 242

DB 2032 PEFAKLLGQAHTTE 2044

RESULT 8

CS3621

probable acid phosphatase PA0190 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 25-Aug-2003

C;Accession: CS3621

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: CS3621

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-241 <STO>

A;Cross-references: GB:AE004457; GB:AE004091; NID:g9946024; PIDN:AAG03580.1; GSPDB:GN001

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA0190

C;Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

Query Match

Best Local Similarity 13.8%; Score 175.5; DB 2; Length 241;

Matches 66; Conservative 41; Mismatches 103; Indels 37; Gaps 10;

QY 8 VCPALFSQALVALVATGNTTTKPDLYLKNSEAINSLALPPPPAVGSIAPLNDQAMY 67

DB 6 LCPSSLCLSLAPLISCLGETAAAP--YPLAHPKPLAD--YLPPLPAADSAADVADLGAV 61

QY 68 EQGLLRNTER-GKLAEDA---NL--SSGGVANAFSGAFSPITEKDPALHKLITNMI 121

DB 62 LEAQRLRTPQVRVRVRAHQEDNVFPAGDLLGSAFKEKRLPLTRS---FNRQENLV 118

QY 122 EDAGDLATRSADHYMRIRPFPAFYGVSTCNTTEQDK----LSKNGSYPSGHTSIGWATLV 177

DB 119 E-----VLMPAKKHFAFRPY-----EVTPKVKVPLPPPEGESYPSGHTMDSYFKAS 165

Query

178 VLAEINPQRQNEILKRGYELGQGRVIVCGYHMQSDVDARFVGSAVVATLHTNPAFCQQQLQ 237
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 166 LLSMLVEHEHDFAFAEAEEHAQSRVLGVHPFDLEGGQTAAALVASLLADPA----- 219
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 238 KAKAEFA 244
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 220 -VAADFA 225
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9

C96991
uncharacterized protein, containing probable phosphatase domain [imported] - Clostridium
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C96991
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; EMID:21359325
A;Accession: C96991
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-591 <Kur>
A;Cross-references: GB:AE001437; PIDK:AAK78718.1; PID:g15023624; GSFPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0742

Query Match

Best Local Similarity 13.1%; Score 167; DB 2; Length 591;
Matches 76; Conservative 41; Mismatches 108; Indels 72; Gaps 14;

Qy 2 KKRVIAVCFAAL----PSSQALALVATGNDTTTKPDLY-YLKSEAINSLALLPPP--PA 54
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 4 KKTFLSALTFLISQSYSVLLARSNGNEITSHAVGYGFVDEWKNNTNNMSPSTNPA 63
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 55 VGSIA-----FINDAQMYEQRLRENT-----ERGLAAEDANLSS----- 90
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 64 IGVLSGYLKLWKPGISYDNGIKLNSDIHLNIQKVIQITVYRTTSFQHQAAYLDORRNQNY 123
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 91 -----GGVANAP---SGAFGSPITE---KDAPALHKLT-----NMIEDAGDL----- 127
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 124 SVLDGLGPYKDAFTKGAGA-GTITDVIPKD--AINVOYTDKGAEGNAEESDSLGSVV 180
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 128 -----ATRASKDHVMRIPPAFYG-VSTCNTTEODKL---SKNGSYSPGHTSIG 172
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 181 KLNVTIERSAASITTPAKYYKYPRPMWSCKVKVPLTVPEKSNPSSDDGGFFSGHTNAA 240
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 173 WATALVLAENIPQRONEILKRGYELGQSRVICGHVHQSDVDARFVGSAVVATLHTN 229
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 241 TICAIALAYAPERYQEMLRASELGNDRIVAGMHPSLDVIGGRWMATAAALNN 297
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10

AB3118
serine proteinase Abu4566 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AB3118
R;Wood, J.W.; Serubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
Xarp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan,
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3118
A>Status: Preliminary
A:Molecule type: DNA
A;Residues: 1-660 <Kur>
A;Cross-references: PTIN:AAU45360.1; PID:g17743054; GSFPDB:GN00187

Query Match 8.3%; Score 105; DB 2; Length 145;
Best Local Similarity 37.5%; Pred. No. 0.055;
Matches 24; Conservative 9; Mismatches 31; Indels 0; Gaps 0;

QY 163 SYSPGHSIGWATLVLAELNPNQNEILKRGYELGQSRVFCVGHWSQVDAARVGSV 222
DB 77 SYSPGHSIGWATLVLAELNPNQNEILKRGYELGQSRVFCVGHWSQVDAARVGSV 136

QY 223 WATL 226
DB 137 ARAL 140

RESULT 13
A87623
PAP2 homolog protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 02-Jun-2003
C:Accession: A87623
R:Kierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, V.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D., J.; Zmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87623
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <S>
A:Cross-references: GB:AE005673; NID:gl3424659; PIDN:AAK24981.1; GSPDB:GN0C148
C:Genetics:
A:Gene: CC3019
C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 7.8%; Score 99.5; DB 2; Length 259;
Best Local Similarity 28.0%; Pred. No. 0.36;
Matches 47; Conservative 15; Mismatches 63; Indels 43; Gaps 5;

QY 88 LSSGVANAFSGAFSGPITEKDAPALHK--LLTNMIEDA----- 124
DB 76 LRVGGQNALVGPDLHVAVDITLGSVAVLTLLIARFALLGLSKRWTEAWLLAIGAL 135

QY 125 -GDLATRSADHYMRIRPFYFVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVL---- 179
DB 136 SGVTVSLSKAVFGRERPDYRVVE-----AVNASPFGHMLSAVVFLTLGVLA 186

QY 180 AEINPNQNEILKRGY-----LQSRVFCVGHWSQVDAARVGSV 221
DB 187 ARFSERRVKILAVSAAYVSVLLVGSRVYLGWHVWSDVLGWSVGA 234

RESULT 14
G39845
dihydroxycarotene dehydrogenase (electron transfer subunit) pyridoxal - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 21-Jul-2000
C:Accession: G39845; D69686
R:Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.
J. Biol. Chem. 266, 9113-9127, 1991
A:Title: Functional organization and nucleotide sequence of the Bacillus subtilis pyrim
A:Reference number: A39845; MUID:91225016; PMID:1709162
A:Accession: G39845
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <Q>
A:Cross-references: GB:MS9757; NID:g4897706; PIDN:AAA21271.1; PID:g143391
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabbet, C.; Ferrati, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Funa, S.; Galizzi, A.; Gallier
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, K.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Toguchi, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.E.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A63580; MUID:98044033; PMID:9384377
A:Accession: D69686
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-256 <KUN>
A:Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13427.1; PID:g2633926
A:Experimental source: strain 168
C:Genetics:
A:Gene: pyrDII
C:Superfamily: Pyrococcus furiosus cytochrome-c3 hydrogenase gamma chain

Query Match 7.6%; Score 96.5; DB 2; Length 256;
Best Local Similarity 22.8%; Pred. No. 0.65;
Matches 65; Conservative 32; Mismatches 105; Indels 83; Gaps 14;

QY 1 MKKRVLAFCFPAALSSQALALVATG---NDTTKEDLYLKNSEALNSLALIP22PPAVGS 57
DB 1 MKKAYLTVCSNQIADRVFQVVLKGLVQGFTPGQFLHLKVSEAVT--PLLRPPIISAD 58

QY 58 IAFINDQA--NY-----EQRLRLNTERGKLAEDANLSSGVAN-----AFSGAFG 102
DB 59 VNFKEVETIYRVDCGTRLLSLKQGLVDVLPLNGFPFVNEVQPKTALLVGGVG 118

QY 103 SPTEKDPALHKLNTNIEDAGD----LATRSADHYMRIRPFYFVSTCNTTEQDKL 158
DB 119 -----VPELQELSKLIEKGVNVIHLGFSAXD-----VFYEBCRGYQGYTYA 163

QY 159 SKNGSYPSGHTSIGWATLV-----VLAEINPNQNEILKRGY-----LQSRVI 203
DB 164 TADGSY--GET--GVTVDIVKXKLEFDLLSCGTPMLKALKQVEYAHKEVLSMERMG 219

QY 204 GYHWSQVDAARVGSVAVATHTN-----PAFQQQ 235
DB 220 CG-----IGACFACVCHNESETSVKVCCLDGPVFKAQ 252

RESULT 15
D82070
conserved hypothetical protein VC2488 [imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Jun-2003
C:Accession: D82070
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
J.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82070
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <HEI>
A:Cross-references: GB:AE004318; GB:AE003852; NID:g9657063; PIDN:AAF95630.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2488
A:Map position: 1
C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 7.5%; Score 96; DB 2; Length 178;
Best Local Similarity 31.0%; Pred. No. 0.44;
Matches 27; Conservative 14; Mismatches 42; Indels 4; Gaps 1;

QY 133 KDHYMRIRPFYFVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPNQNEILK 192

Db 81 KNSFQRRRPOELSAEVTAYITPSDRY----SLESGHTAAAFVMAATLIGYIYPHWYAVALC 136

Qy 193 RGYELGQSRVICGYHWCSDVDARVWG 219

Db 137 WAGLIGLARVLLGVHFLSDVIAGALLG 163

Search completed: June 2, 2004, 10:47:30
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: June 2, 2004, 10:39:23 ; Search time 18 Seconds
[without alignments]
720.304 Million cell updates/sec

Title: US-09-807-990-2
Perfect score: 1276
Sequence: 1 MKGVV...CPAALFSSQALA.....PAFOOQLQKAKAEPAHQXK 249
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	
1	1014	79.5	249	1	PHOC MORMO	P28581 morganella
2	1013	79.4	248	1	PHON PROST	P26975 providencia
3	486	38.1	250	1	PHON SALTY	P26976 salmonella
4	477	37.4	250	1	PHON SALTY	Q934J6 salmonella
5	339.5	26.6	264	1	PPA ZYMOM	P14924 zymomonas m
6	96.5	7.6	256	1	PYRK BACSU	P25983 bacillus su
7	96	7.5	809	1	HRPB_ECOLI	P37024 escherichia
8	89.5	7.0	1157	1	PEX1_PICPA	P46463 picchia past
9	88	6.9	921	1	NAC2 HUMAN	Q9UPR5 homo sapien
10	86.5	6.8	390	1	TSDF_BRUSU	Q9G0H4 b ispd/ispf
11	86	6.7	725	1	RNR_MYCPU	Q98Q10 mycoplasma
12	86	6.7	1573	1	AROI SCHPO	Q9P7R0 s pentafunc
13	85.5	6.7	390	1	ISDF BRUME	Q8YH8 b ispd/ispf
14	85	6.7	1603	1	ESC DROME	P35820 drosophila
15	82.5	6.5	561	1	VGLF SV41	P25181 simian viru
16	82.5	6.5	898	1	UBPE_DROME	Q24574 drosophila
17	82.5	6.5	921	1	NAC2 RAT	Q87688 rattus norv
18	81.5	6.4	455	1	ODO2 PIG	Q9N0F1 sus scrofa
19	81.5	6.4	2796	1	CSM3 MOUSE	Q80T79 mus musculu
20	81.5	6.4	3670	1	CSM3 HUMAN	Q72407 homo sapien
21	80.5	6.3	473	1	HN3A HUMAN	P55317 homo sapien
22	80.5	6.3	486	1	YU69_YERPE	Q8ZCC3 yersinia pe
23	80.5	6.3	2206	1	POLG_POL3L	P03302 poliovirus
24	80	6.3	301	1	MPEV SYNEY	Q21178 synechococc
25	80	6.3	376	1	MURG RICCQ	Q92158 rickettsia
26	80	6.3	511	1	PUR9_SUNY3	P74741 s bifunctio
27	80	6.3	953	1	FN33 MOUSE	Q9R1C7 mus musculu
28	79.5	6.2	232	1	XDBE_ECOLI	Q46800 escherichia
29	79.5	6.2	453	1	ODO2 HUMAN	P36957 homo sapien
30	79.5	6.2	732	1	POK DROME	Q01842 drosophila
31	79.5	6.2	750	1	YKS7 YEAST	P34231 saccharomyc
32	79.5	6.2	3746	1	ACVS_PENCH	P19787 penicillium
33	79.5	6.2	3791	1	ACVT_PENCH	P26046 penicillium

RESULT 1
PHOC MORMO
ID PHOC MORMO STANDARD; PRT; 249 AA.
AC P28581;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Major phosphate-irrepressible acid phosphatase precursor (EC 3.1.3.2)
DE (HPAP).
GN PHOC.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-40.
RC STRAIN=RS12;
RX MEDLINE=94362901; PubMed=3081499;
RA Thaller M.C., Berlutti F., Schippa S., Lombardi G., Rossolini G.M.;
RT "Characterization and sequence of Phoc, the principal phosphate-
irrepressible acid phosphatase of Morganella morganii.";
RL Microbiology 140:1341-1350(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 10466;
RX MEDLINE=20336426; PubMed=10877772;
RA Mihara Y., Utagawa T., Yamada H., Asano Y.;
RT "Phosphorylation of nucleosides by the mutated acid phosphatase from
Morganella morganii.";
RL Appl. Environ. Microbiol. 66:2811-2816(2000).
CC -!- FUNCTION: HAS A PH OPTIMUM AROUND 6.
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
alcohol + phosphate.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: Belongs to the class A bacterial acid phosphatase
family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X64444; CAA45774.1; -;
CC EMBL; AB035805; BAA96744.1; -;
CC PIR; S19187; S19187.
CC InterPro; IPR008934; ACPase_VanPerase.
CC InterPro; IPR001011; Bac_AcPaseA.
CC InterPro; IPR000326; PA_PTPase.
CC Pfam; PF01569; PAP2; 1.
CC PRINTS; PR00483; BACPHPTASE.
CC ProDom; PD009838; Bac_AcPaseA; 1.
CC SMART; SM00014; acidPpC; 1.

DR PROSITE; PS01157; ACID PHOSPH CL A; 1.
 KW Hydrolase; Periplasmic; Signal.
 FT SIGNAL 1 20
 CHAIN 21 249 MAJOR PHOSPHATE-IRREPRESSIBLE ACID
 SEQUENCE 249 AA; 26998 MW; C43F3698052B6A5C CRC54;
 Query Match 79.5%; Score 1014; DB 1; Length 249;
 Best Local Similarity 77.1%; Pred. No. 7.3e-83;
 Matches 192; Conservative 23; Mismatches 34; Indels 0; Gaps 0;

QY 1 MKKRVAVCTAALFSSCALALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
 DB 1 MKKRVAVCTAALFSSCALALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
 QY 61 LNDQMYEQGLRNTERRGKLAADANLSSGGVANAFSGAFGSPITEKDAPELHKLITNM 120
 DB 61 LNDQMYEQGLRNTERRGKLAADANLSSGGVANAFSGAFGSPITEKDAPELHKLITNM 120
 QY 121 IEDAGDLATRSADKHMYRIRPFYGVSTCNTTQDKLXNGSYPSGHTSIGWATALVLA 180
 DB 121 IEDAGDLATRSADKHMYRIRPFYGVSTCNTTQDKLXNGSYPSGHTSIGWATALVLA 180
 QY 181 EIMPQONEILKGYELGQSRVCGYHWSQDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
 DB 181 EIMPQONEILKGYELGQSRVCGYHWSQDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
 QY 241 AEFQHQK 249
 DB 241 QEFQKQK 249

RESULT 2

PEON PROST
 ID PHON PROST STANDARD; PRT; 248 AA.
 AC E26975;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
 GN PHON.
 OS Providencia stuartii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Providencia.
 OX NCBI_TaxID=588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PV81;
 RA Riccio M.L., Lombardi G., Chiesurin A., Satta G.;
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 CC -|- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC -|- SUBCELLULAR LOCATION: Periplasmic.
 CC -|- SIMILARITY: Belongs to the class A bacterial acid phosphatase
 CC family.
 CC
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 CC
 CC EMBL; X64820; CAA46032.1; -
 CC DR E19868; PACFCS.
 DR InterPro; IPR008934; AcPase VanPerase.
 DR InterPro; IPR010111; BacAcPaseA.
 DR InterPro; IPR000326; PAFrase.
 DR Pfam; PF01569; PAP2; 1.
 DR PRINTS; PR03483; BACPDPHTASE.
 DR ProDom; PD009836; BacAcPaseA; 1.
 DR SMART; SMC0014; acidPPc; 1.

DR PROSITE; PS01157; ACID PHOSPH CL A; 1.
 KW Hydrolase; Periplasmic; Signal.
 FT SIGNAL 1 20
 CHAIN 21 248 NONSPECIFIC ACID PHOSPHATASE.
 SEQUENCE 248 AA; 27043 MW; 2122A4B95E767CB2 CRC64;
 Query Match 79.4%; Score 1013; DB 1; Length 248;
 Best Local Similarity 77.4%; Pred. No. 9e-83;
 Matches 192; Conservative 26; Mismatches 30; Indels 0; Gaps 0;

QY 1 MKKRVAVCTAALFSSCALALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
 DB 1 MKKRVAVCTAALFSSCALALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
 QY 61 LNDQMYEQGLRNTERRGKLAADANLSSGGVANAFSGAFGSPITEKDAPELHKLITNM 120
 DB 61 LNDQMYEQGLRNTERRGKLAADANLSSGGVANAFSGAFGSPITEKDAPELHKLITNM 120
 QY 121 IEDAGDLATRSADKHMYRIRPFYGVSTCNTTQDKLXNGSYPSGHTSIGWATALVLA 180
 DB 121 IEDAGDLATRSADKHMYRIRPFYGVSTCNTTQDKLXNGSYPSGHTSIGWATALVLA 180
 QY 181 EIMPQONEILKGYELGQSRVCGYHWSQDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
 DB 181 EIMPQONEILKGYELGQSRVCGYHWSQDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
 QY 241 AEFQHQK 248
 DB 241 DEFQKQK 248

RESULT 3

PHON SALTY
 ID PHON SALTY STANDARD; PRT; 250 AA.
 AC P26976;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
 GN PHON OR STM4319.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14028;
 RA Groisman E.A., Saier M.H. Jr., Ochman H.;
 RL "Horizontal transfer of a phosphatase gene as evidence for mosaic
 RL structure of the Salmonella genome.";
 RL EMBO J. 11:1309-1316(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RA MEDLINE=92041557; PubMed=1938882;
 RA Kasahara M., Nakata A., Shinagawa H.;
 RL "Molecular analysis of the Salmonella typhimurium phoN gene, which
 RL encodes nonspecific acid phosphatase.";
 RL J. Bacteriol. 173:6760-6765(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RA MEDLINE=21534949; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Dante M., Du F., Hou S., Layman D.,
 RA Courtney L., Porwollik S., Ali J., Holmes A., Grewal N., Mulvaney E.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Miller W., Stoneking T., Nhan M.,
 RA Ryan E., Sun H., Florea L., Miller W., Wilson R.K.;
 RL "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RL LT2.";
 RL Nature 413:852-856(2001).
 CC -|- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an

```

CC alcohol + phosphate.
CC -!- SUBUNIT: Homodimer (Probable).
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: Belongs to the class A bacterial acid phosphatase
CC family.
CC -!- CAUTION: Ref.2 sequence differs from that shown in the C-terminus
CC due to a frameshift.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X63599; CAA45144.1; -.
DR EMBL; X59036; CAA41760.1; ALT_FRAME.
DR EMBL; AE008902; AAL23143.1; -.
DR PIR; S20958; A41330.
DR StyGene; SG10292; phoN.
DR InterPro; IPR008934; AcPase VanPerase.
DR InterPro; IPR001011; Bac AcPaseA.
DR InterPro; IPR000326; PA_PTPase.
DR Pfam; PF01563; PAP2; 1.
DR PRINTS; PR02483; BACPHPTASE.
DR PRODOM; PD003838; Bac AcPaseA; 1.
DR SMART; SM00014; acidPPc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CLA; 1.
KW Hydrolase; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 250 NONSPECIFIC ACID PHOSPHATASE.
SQ SEQUENCE 250 AA; 28382 MW; CFE8DA4095D57573 CRC64;
Query Match 38.1%; Score 486; DB 1; Length 250;
Best Local Similarity 43.0%; Pred. No. 5.3e-36;
Matches 104; Conservative 33; Mismatches 99; Indels 10; Gaps 2;
Qy 1 MKKRLVAVCFALFSSQALALVATGNDTTTKPOLYLNKNSAINSLALLPPPPAVGSIAP 60
Db 1 MRSRYLVPFLFLIVAKYTSA-----ETVQP---FHSPESVNSQFVLPFGNDPAP 50
Qy 61 LNDQAMVEQGLLRNTERGKLAEDANLSSGGVANAFSGAFGSPITEKDAIPALHKLINM 120
Db 51 RYDEAYVFKGYAIGKSPRWKQAEADVSVENIARIFSPVVGAKINPKDTPETWMLKNL 110
Qy 121 IEDAGDLATRSADKHMYRIRPFYFVGVTGNTTQDQLSKNGSPSGHTSIGWATLVLA 180
Db 111 LTWGGYATASAKYMYRTREPVLFNHSCTPEDETLRKNGSPSGHTIAYGTLIALVLS 170
Qy 181 EINPQRNEILKRGYELGOSRVICGYHMQSDVDAARVVGSAVVATLTNTPAFQOQLOKAK 240
Db 171 EARDPRAQELARRGWETFGQSRVICGAIHWQSDVDAGRYVGAVEFARLQTIPIAFQSLAKVR 230
Qy 241 AE 242
Db 231 EE 232
RESULT 4
PHON SALT1
ID PHON_SALT1 STANDARD; PRT; 250 AA.
AC Q934J6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
GN PHON OR STY4519 CR T4225.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=601;
RN [1]

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RP SEQUENCE FROM N.A.
RA Rao A.S., Mukhopadhyaya R., Mahajan S.K.;
RT "phoN, a gene for acid phosphatase from Salmonella typhi.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the class A bacterial acid phosphatase
CC family.
CC -----
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CC -----
DR EMBL; AF366353; AAKS0861.1; -.
DR EMBL; AL627282; CAD09303.1; -.
DR EMBL; AE016848; AAO71687.1; -.
DR InterPro; IPR008934; AcPase VanPerase.
DR InterPro; IPR001011; Bac AcPaseA.
DR InterPro; IPR000326; PA_PTPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODOM; PD009838; Bac AcPaseA; 1.
DR SMART; SM00014; acidPPc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CLA; 1.
KW Hydrolase; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 250 NONSPECIFIC ACID PHOSPHATASE.
SQ SEQUENCE 250 AA; 28459 MW; 02B92D2035F4FE82 CRC64;
Query Match 37.4%; Score 477; DB 1; Length 250;
Best Local Similarity 47.0%; Pred. No. 4e-35;
Matches 95; Conservative 31; Mismatches 76; Indels 0; Gaps 0;
Qy 41 EAINSLALLPPPPAVGSIAPFLNDQAMVEQGLLRNTERGKLAEDANLSSGGVANAFSGA 100
Db 31 ESVNSQFVLPFGNDPAPFYDYKEAYFKGYAIGKSPRWKQAEADISVENIARIFSPV 90
Qy 101 FGSPITEKDAIPALHKLINMIEDAGDLATRSADKHMYRIRPFYFVGVTGNTTEQDKLSK 160
Db 91 VGAKINPKDTPETWMLKNLQMLKMGYYATASAKYMYRTREPVLFNHSCTPEDETLRK 150
Qy 161 NGSYPSGHTSIGWATLVLAENPQRNEILKRGYELGOSRVICGYHMQSDVDAARVVG 220
RN [1]

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KAHLER A.E., Nielsen F.S., Switzer R.L.;
"Biochemical characterization of the heteromeric Bacillus subtilis
dihydroxycarboxylate dehydrogenase and its isolated subunits";
Arch. Biochem. Biophys. 371:191-201(1999).
CC -!- FUNCTION: Is responsible for channeling the electrons from the
oxidation of dihydroxycarboxylate from the FMN redox center in the pyrid
subunit to the ultimate electron acceptor NAD(+).
CC -!- COFACTOR: Binds 1 2Fe-2S cluster and 1 PAD per subunit.
CC -!- PATHWAY: Pyrimidine biosynthesis; fourth step.
CC -!- SUBUNIT: Heterotetramer of 2 pyrk and 2 pyrd subunits.
CC -!- SIMILARITY: Belongs to the pyrk family.
CC
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CC
EMBL; M59757; AAA21271.1; -;
DR EMBL; Z99112; CAB13427.1; -;
DR PIR; G39845; G39845.
DR Subtilist; BG10717; pyrk.
DR HAMAP; MF 01211; -; 1.
DR InterPro; IPR006058; 2Fe2S fd BS.
DR InterPro; IPR001433; Oxred_FAD/NAD (P).
DR Pfam; PF00175; NAD binding_1; 1.
DR PROSITE; PS0197; 2FE2S_FERREDOXIN; FALSE NEG.
KW Pyrimidine biosynthesis; transport; Electron transport; Metal-binding;
KW Iron; iron-sulfur; 2Fe-2S; Flavoprotein; FAD; Complete proteome.
FT METAL 220 IRON-SULFUR 1 (2FE-2S) (PROBABLE).
FT METAL 225 IRON-SULFUR 1 (2FE-2S) (PROBABLE).
FT METAL 228 IRON-SULFUR 2 (2FE-2S) (PROBABLE).
FT METAL 243 IRON-SULFUR 2 (2FE-2S) (PROBABLE).
FT METAL 243 IRON-SULFUR 2 (2FE-2S) (PROBABLE).
SQ SEQUENCE 256 AA; 28099 MW; DC7B7605E39C2E15 CRC64;
Query Match 7.6%; Score 96.5; DB 1; Length 256;
Best Local Similarity 22.8%; Pred. No. 0.27;
Matches 65; Conservative 32; Mismatches 105; Indels 83; Gaps 14;
QY 1 MKKRVLAFCFAALPSSQALVALVATG---NDTTPEDLYLKNSEAINSLALLPPPPAVCS 57
DB 1 MKKAYLTVCNSQIADRFVFMVKGELVQGTTPGQFLHLKVSEAVT--PLLRRPISIA 58
QY 58 IAFLENDQA--MY-----EQGLLRNTERCKLAEDANLSSGGVAN-----AFSGAFG 102
DB 59 VNFKEVETIYRVGEGTRLLSKQQGLVDVJLGLNGFPVNEVQPKALLVGGVG 118
QY 103 SPITEKDALHLLTNMIEDAGD---LATASAKDHYMRIRPFYGVSTNTTEQDKL 158
DB 119 -----VPPQLQELSKRLIEKGVNVIHVLGFQSAKD-----VFYEBCRQYGDYVA 163
QY 159 SSKSYSGHTSIGWATL-----VLAEINPQRONEILKQYE-----LQQRVVI 203
DB 164 TADGSY--GET--GEVTIVIRKKLEFDILLSGCGPTMKALKQYAHKVVYLSMEERM 219
QY 204 CGYHQSDVDAARVVGSAVATLTNT-----PAFQQQ 235
DB 220 CG-----IGACFACVCHTNESETSYKVCILGVPFKAQ 252
RESULT 7
ID HRPB_ECOLI STANDARD; PRT; 8C9 AA.
AC P37024; P75663;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP-dependent helicase hrpB.
GN HRPB OR B0148.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94261430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishihama A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
the 2.4-4.1 min (110,917-193,643 bp) region.";
RL Nucleic Acids Res. 22:1637-1639(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE OF 61-156 FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=95206938; PubMed=7899078;
RA Moriya H., Kasai H., Isono K.;
RT "Cloning and characterization of the hrpA gene in the terC region of
Escherichia coli that is highly similar to the DEAH family RNA
helicase genes of Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 23:595-598(1995).
CC -!- SIMILARITY: TO EUKARYOTIC RNA HELICASES; STRONGEST SIMILARITY
TO YEAST DHR.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to
frameshifts.
CC
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CC
EMBL; D26562; -; NOT ANNOTATED CDS.
DR EMBL; AE000124; AAC73259.1; ALT_INIT.
DR EMBL; D42122; BAA21040.1; -;
DR EcoGene; EG12329; hrpB.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007502; Helicase_dom.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF04408; HA2; 1.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM02487; DEXDC; 1.
DR SMART; SM02490; HELICC; 1.
KW Helicase; ATP-binding; Complete proteome.
FT NP_BIND 27 34 ATP (POTENTIAL).
FT SITE 123 126 DEFB BOX.
SQ SEQUENCE 809 AA; 89147 MW; 413605E1D2D90715 CRC64;
Query Match 7.5%; Score 96; DB 1; Length 809;
Best Local Similarity 23.2%; Pred. No. 1.3;
Matches 66; Conservative 33; Mismatches 116; Indels 70; Gaps 13;
QY 3 KRVLAFCFA--ALPSSQALVALVATGNDT--TKPDLYLKNSE-----AINSLALLPPPPAV 55
DB 390 KRLQMLGALGERLSAQCKMAALGNDPRLAAMLVSAKNDDEAATAKIALLEPERM 449
QY 56 GS-----IAPLNDQAMYEQ--GRLLNTERGKLAEDANLSSGGVANAFSGAFGSPITEKD 109
DB 450 GNSDVGAFVSRNOPAWQCRSQQLK-----RLNVRGGEADSLIAPLLAGAFADRIARR 504
QY 110 APALHLLTN--MIEDAGDLATRSKADHYMRIRPFYGV-----146

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Db 505 GQDGRYQLAKMGAMLDANDALSR-----HEWLIAPLLQLQGSAPDARILALALYIDIDELV 560
Qy 147 -----YSTNTTFOCKLXKNGSVPS-GHTSIGWATLV--LA-----EINPQONEILX 192
Db 561 QRCPLVQSDTVZWD--DAQGTIKAWRLQIGQITVKVQPLAKPSEDELEQAMLINGIRD 618
Qy 193 RGY-----ELGQSRVIGYHQSDVDAARVVGSAAVATLHT 228
Db 619 KGLSVLWNTAAEQRLRLLCARWLPDYDWPVADDESLLAALET 663

RESULT 8
PEX1_PICPA
ID PEX1_PICPA STANDARD; PRT; 1157 AA.
AC P46463;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Peroxisome biosynthesis protein PEX1 (Peroxin-1).
GN PEX1 OR PEX1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21-1;
RX MEDLINE=95050987; PubMed=7962088;
RA Heyman J.A., Monosov E., Subramani S.;
RT "Role of the PEX1 gene of Pichia pastoris in peroxisome biogenesis.";
RL J. Cell Biochem. 127:1259-1273(1994).
CC -!- FUNCTION: Involved in peroxisome biosynthesis. May play a direct
CC or indirect role in delivering membrane material to developing
CC peroxisomes. It may also be involved in intracellular membrane
CC movement.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the AAA ATPase family.

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EMBL: Z36987; CA885450.1; -.
DR PIR; A55152; AAA_ATPase.
DR InterPro; IPR003593; AAA_ATPase_Centr.
DR InterPro; IPR003959; AAA_ATPase_Centr.
DR Pfam; PF00004; AAA; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00674; AAA; 1.
KW Peroxisome; ATP-binding; Repeat.
FT NP_BIND 523 530 ATP (POTENTIAL).
FT NP_BIND 940 947 ATP (POTENTIAL).
SQ SEQUENCE 1157 AA; 126984 MW; B26F46F55A92DA3C CRC64;

Query Match 7.0%; Score 89.5; DB 1; Length 1157;
Best Local Similarity 21.2%; Pred. No. 8.1; Indels 79; Gaps 12;
Matches 55; Conservative 40; Mismatches 86;

Qy 25 GNDTTTKPD-----LYLKNSEAINSLALPPPPVGVSTAFNDQAMYEQGRLL----- 72
Db 909 GHDSGTGTVDRVWQMLQMDAGELDGYYVL---AATSREPLDLSALLRPGRLDKSVIC 964
Qy 73 -----LRNTERGKLAEDANLSS-GGVANAFSGAPGSPITEKQAPAL----- 113
Db 965 DMPDFDRELDILQSVTRNMYKSVNLSSVAGSGSGFSGA-----DLQALAYNAYLK 1016
Qy 114 --HKLLR--NNIEDAGDLATSAKDHYRIEPPAFYGVSTCTTTEQDKLSKNGSVPSGHT 169
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Db 1017 AVHEKLLKDESMAMAGEDDND--DKRMVSCFOFSG-----NTEKKS----- 1057
Qy 170 SIGWATLVLAERINPQRONEILKRGYELGQSRVIGYHQSDVDAARVVGSAAVATLHTN 229
Db 1058 -----LIELKPSDRATVKKLEHLYQGN---GNHAEGET-KSKLATTANSVIITS 1104
Qy 230 PAFQOQLQXAKAEFAHQKK 249
Db 1105 KDFEDSLSETKQISQSEKR 1124

RESULT 9
NAC2_HUMAN
ID NAC2_HUMAN STANDARD; PRT; 921 AA.
AC Q9UPR5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
DE 2).
GN SLC8A2 OR NCX2 OR KIAA1087.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99397452; PubMed=10470851;
RA Kituno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N.,
RA Tanaka A., Kofani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:197-205(1999).
CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC coupling. Ca(2+) is extruded from the cell during relaxation so as
CC to prevent overloading of intracellular stores (By similarity).
CC -!- ENZYME REGULATION: By ATP (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

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EMBL: AB029010; BAA83039.1; ALT_INIT.
DR Genbank; HGNC:11069; SLC8A2.
DR MIW; 601901; -.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004836; Na_Ca_Ex.
DR InterPro; IPR004837; NaCa_Exmemb.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRfams; TIGR00845; caca; 1.
KW Transport; Antiport; Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 921 SODIUM/CALCIUM EXCHANGER 2.
FT DOMAIN 21 68 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 69 90 POTENTIAL.
FT DOMAIN 91 130 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 131 152 POTENTIAL.
FT DOMAIN 153 164 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 165 185 POTENTIAL.
FT DOMAIN 186 196 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 197 219 POTENTIAL.
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KW Multifunctional enzyme: Complete proteome.
FT DOMAIN 1 226 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL
FT FT 227 390 2-C-METHYL-D-ERYTHRITOL 2,4-
FT FT 390 41839 MW; 05AB0A2FBA03DEDB CRC64;
SQ SEQUENCE 390 AA; 41839 MW; 77024F4097736473 CRC64;

Query Match 6.7%; Score 85.5; DB 1; Length 390;
Best Local Similarity 19.0%; Pred. No. 4.4;
Matches 58; Conservative 48; Mismatches 102; Indels 97; Gaps 14;

QY 32 PDLYLKNSEAI--NSLALPPPPAVGSIAL--NQAMYEQGRLLNTERGKLAEDA 86
DB 16 PKQYRLIGAELARTLRAFTDCPLIGTIAVPHDPDHALYRRRAVPEKH-----ENV 67
QY 87 NLSGGVANAFSGAFSPITEKAP-----ALHKLNTNMIEDAG----- 125
DB 58 LVVGGTRQESTRLGLLAKDEAPQVYLHDGVRPTFGQDLLEIRIANLTFNGVLPAL 127
QY 126 ---DLATRSKDHVYRI-----RPAF-----YGVSTNTTEQDKLS 159
DB 128 AVSDTLKRAAAGMVGVTTSRTGLFACTPQAFTYAPILDAHEKAFAINRTDFTDDAIA 187
QY 160 K-----NGSPSGHTSGNATLVLAELNFORQNEILK-----RGYEL-----GQS 200
DB 188 EWQEIYAVRIEIGS--ADNTKLNTAKDIEMADKRLURQDHAVFPDRTGNGYDVHISFEPGDH 245
QY 201 RVTCG-----YHWQSDVDAA--RVGSGAVVAT-----LHTNPAFOOQLQKAKAEFA 244
DB 246 VTLCGVKIPHEAKLNGHSDADVALHALTDALLATRGADGICTGTFPPSPDPQWKGASRIFI 305
QY 245 QHCKK 249
DB 306 EHAAK 310

RESULT 14
PSC DROME STANDARD; PRT; 1603 AA.
ID PSC DROME STANDARD; PRT; 1603 AA.
AC P35820;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Posterior sex combs protein.
GN PSC.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RF SEQUENCE FROM N.A.
RX MEDLINE=92018190; PubMed=1833647;
RA Brunk B.P., Martin E.C., Sharp E., Adler P.N.;
RT "Drosophila genes Posterior Sex Combs and Suppressor two of zeste
RL Nature 353:351-353(1991).
CC -!- FUNCTION: The Polycomb group (Pc-G) genes are needed to maintain
CC expression patterns of the homeotic selector genes of the
CC antennapedia (Antp-C) and bithorax (Bx-C) complexes, and hence for
CC the maintenance of segmental determination.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; X59275; CAA41965.1; --
```

```
DR PIR; S17983; S17983.
DR FlyBase; FBgn0005634; Psc.
DR InterPro; IPR001841; Znf.ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KM Zinc-finger; Developmental protein; DNA-binding; Nuclear protein.
FT DOMAIN 47 53 POLY-THR.
FT DOMAIN 83 88 POLY-THR.
FT DOMAIN 91 98 POLY-THR.
FT DOMAIN 145 152 POLY-THR.
FT DOMAIN 184 202 POLY-SER.
FT ZN FING 265 304 RING-TYPE.
FT DOMAIN 642 651 POLY-SER.
FT DOMAIN 1066 1069 POLY-GLY.
FT DOMAIN 1185 1189 POLY-PRO.
FT DOMAIN 1214 1217 POLY-PRO.
FT DOMAIN 1391 1396 POLY-PRO.
FT DOMAIN 1458 1461 POLY-ALA.
FT DOMAIN 1517 1520 POLY-GLY.
SQ SEQUENCE 1603 AA; 169999 MW; 77024F4097736473 CRC64;

Query Match 6.7%; Score 85; DB 1; Length 1603;
Best Local Similarity 20.7%; Pred. No. 31;
Matches 50; Conservative 29; Mismatches 78; Indels 84; Gaps 8;

QY 1 MKKRLVAVCFEALPSSQALALVATG-----NDTTTKPDLYLKNSEAI--NSLALPP 51
DB 115 LKQQLFRACSIKVKSENALATTATAALAAATTTTATPALATGKAATILENGIKKEST 174
QY 52 PPAVGSIAFLNDQAMYEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKAP 111
DB 175 PPAVESV-----EASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 208
QY 112 ALHKLLTNMIEDAGDLATRSKDHVYRIKRPFAFYGVSTCNTTEQDKLKNGSYPSGHTSI 171
DB 209 S-----EDASSNGGASDEKSEEDPRAVAASTATITSLATTSRPP----- 253
QY 172 GWATLVLAELNFORQNEILKRGVYELGQSRVIC---GYHWQSDVDAAARVVGSAVATLH 227
DB 254 -----VLLTAVNP-----HICHLCQGY-----LINATTIVECLH 283
QY 228 T 228
DB 284 S 284

RESULT 15
VGLF SV41 STANDARD; PRT; 561 AA.
ID VGLF SV41 STANDARD; PRT; 561 AA.
AC P25181;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
GN Fusion glycoprotein F1].
OS Simian virus 41 (SV41).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11228;
RN [1]
RF SEQUENCE FROM N.A.
RX STRAIN=Toshiiba/Chanock;
RX MEDLINE=91049440; PubMed=2173260;
RA Tsurudome M., Bando H., Nishio M., Iwamoto Y., Kawano M., Kondo K.,
RA Komada H., Ito Y.;
RT "Antigenic and structural properties of a paramyxovirus simian virus
RT 41 (SV41) reveal a close relationship with human parainfluenza type 2
RT virus.";
RL Virology 179:738-748(1990).
RN [2]
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 10:38:48 ; Search time 61 Seconds
(without alignments)
1153.350 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKREVLAVCAALFSSQALA.....PAFQQQLQKAKAEFAQHKK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1276	100.0	249	2 AAW06463	AAW06463 Escherich
2	1276	100.0	249	2 AAW71029	AAW71029 Acid phos
3	1276	100.0	249	4 AAB75066	AAB75066 Escherich
4	1183	92.7	231	2 AAW71034	AAW71034 Mutant ac
5	1178	92.3	231	2 AAW71035	AAW71035 Mutant ac
6	1161	91.0	231	2 AAW71036	AAW71036 Mutant ac
7	1158	90.8	248	2 AAW06458	AAW06458 Enterobac
8	1158	90.8	248	2 AAW71031	AAW71031 Acid phos
9	1155	90.5	231	2 AAW71037	AAW71037 Mutant ac
10	1152	90.3	231	2 AAW71038	AAW71038 Mutant ac
11	1143	89.6	248	2 AAW06459	AAW06459 Klebeieil
12	1143	89.6	248	2 AAW71032	AAW71032 Acid phos
13	1141	89.4	231	2 AAW71039	AAW71039 Mutant ac
14	1137	89.1	231	2 AAW71040	AAW71040 Mutant ac
15	1133	88.8	231	2 AAW71041	AAW71041 Mutant ac
16	1129	88.5	231	2 AAW71042	AAW71042 Mutant ac
17	1112	87.1	248	4 AAB75068	AAB75068 Enterobac
18	1014	79.5	249	2 AAW06462	AAW06462 Morganell
19	1014	79.5	249	2 AAW71028	AAW71028 Acid phos
20	1014	79.5	249	4 AAB75065	AAB75065 Morganell
21	1013	79.4	248	2 AAW06457	AAW06457 Providenc
22	1013	79.4	248	2 AAW71030	AAW71030 Acid phos
23	973	76.3	249	4 AAU27583	AAU27583 Fusion pr
24	780	61.1	244	2 AAW06460	AAW06460 Serratia
25	780	61.1	244	2 AAW71033	AAW71033 Acid phos

26	591	46.3	246	2 AAR54082	AAR54082 Virulence
27	586	45.9	246	2 AAR35759	AAR35759 Apryrase
28	481	37.7	232	4 AAB75066	AAB75066 Salmonell
29	339.5	26.6	264	4 AAB75067	AAB75067 Zymomonas
30	314.5	24.6	252	2 AAR20014	AAR20014 Ascorbic
31	149.5	11.7	508	4 AAU56365	AAU56365 Propionib
32	149.5	11.7	508	6 AAB52884	AAB52884 Propionib
33	143	11.2	622	4 AAG91063	AAG91063 C glutami
34	130.5	10.2	513	5 AAB65275	AAB65275 Bifidobac
35	105	8.2	58	5 ABP08795	ABP08795 Human ORF
36	96	7.5	178	6 ABU49566	ABU49566 Protein e
37	96	7.5	824	4 AAG98907	AAG98907 E. coli g
38	96	7.5	824	6 ABU14676	ABU14676 Protein e
39	95	7.4	855	4 AAG29301	AAG29301 Novel hum
40	93.5	7.3	704	6 ABB80170	ABB80170 A. fumiga
41	92.5	7.2	159	4 AAB76560	AAB76560 Corynebac
42	92.5	7.2	159	4 AAG92925	AAG92925 C glutami
43	92	7.2	398	6 AAW70672	AAW70672 Photorhab
44	90.5	7.1	437	6 AAB38661	AAB38661 Protein e
45	90.5	7.1	578	4 ABB71754	ABB71754 Drosophil

ALIGNMENTS

RESULT 1
AAW06463
ID AAW06463 standard; protein; 249 AA.
AC AAW06463;
XX
XX 13-AUG-1997 (first entry)
XX
DE Escherichia blattae JCM 1650 acid phosphatase.
XX
XX JCM 1650; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
KW condiment; pharmaceutical; intermediate.
XX
OS Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT Peptide /label= sig_peptide
FT Peptide 19..249
FT Misc-difference 92 /label= mat_peptide
FT /note= "optionally replaced by another amino acid"
FT Misc-difference 171 /note= "optionally replaced by another amino acid"

WO9637603-A1.

28-NOV-1996.

24-MAY-1996; 96WO-JP001402.

25-MAY-1995; 95JP-00149781.

26-MAR-1996; 96JP-00094680.

(AJIN) AJINOMOTO CO INC.

Mihara Y, Utagawa T, Yamada H, Asano Y;

WPI; 1997-021215/02.

N-PSDB; AAT45011.

Efficient production of nucleoside 5'-phosphate - by reaction of a nucleoside with a phosphoric acid donor in the presence of an acid phosphatase.

Claim 3; Page 56-58; 95pp; Japanese.

The present sequence is the Escherichia blattae JCM 1650 acid phosphatase

CC (AP), which can be used to produce a nucleoside 5'-phosphate ester from
 CC the corresponding nucleoside when a phosphate donor, e.g. poly-, phenyl-
 CC or carbamyl-phosphoric acid, is reacted in its presence at pH 3.0 to 5.5.
 CC The PA can be used for the economic and efficient production of
 CC nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals and
 CC intermediates for pharmaceuticals

XX Sequence 249 AA;

Query Match 100.0%; Score 1276; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKRVLAFCFAALFSSQALALVATGNTTTKPDLYLYLKNSEAINSLALLPPPPAVGSI AF 60
 DB 1 MKKRVLAFCFAALFSSQALALVATGNTTTKPDLYLYLKNSEAINSLALLPPPPAVGSI AF 60
 QY 61 LNPQAMYEQGRLLRNTGRKLAEDANLSSGGVANAFSGAFSPITRKDAPALHKLITNM 120
 DB 61 LNPQAMYEQGRLLRNTGRKLAEDANLSSGGVANAFSGAFSPITRKDAPALHKLITNM 120
 QY 121 IEDAGDLATRSKADHYRIIRPFAYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
 DB 121 IEDAGDLATRSKADHYRIIRPFAYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
 QY 181 EINPQRONEILKRGYELGQSRVIGYHWSQSDVDARVVGSAVATLTNPAFQOOLQKAK 240
 DB 181 EINPQRONEILKRGYELGQSRVIGYHWSQSDVDARVVGSAVATLTNPAFQOOLQKAK 240
 QY 241 AEFAQHOKK 249
 DB 241 AEFAQHOKK 249

RESULT 2

AAW71029
 ID AAW71029 standard; protein; 249 AA.
 AC AAW71029;
 XX
 XX 21-OCT-1998 (first entry)

DE Acid phosphatase enzyme amino acid sequence.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KW intermediate.

XX Escherichia blattae.

XX Key Location/Qualifiers
 FE Peptide 1..18
 FT /note= "signal peptide"
 FT P-Protein 19..249
 FT /note= "mature protein; Claim 6"

XX EP857788-A2.

XX 12-AUG-1998.

XX 20-NOV-1997; 97EP-00309165.

XX 21-NOV-1996; 96JP-00311103.

XX 18-JUN-1997; 97JP-00161674.

XX (AJIN) AJINOMOTO CO INC.

XX Mihara Y, Utagawa T, Yamada H, Asano Y;

XX WPI; 1998-416010/36.

XX N-PSDB; AAV43046.

XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings

or pharmaceutical intermediates.

XX Example 12; Page 35-36; 83pp; English.

CC The present sequence represents an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC that has been transformed with recombinant DNA containing a gene coding
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them

XX Sequence 249 AA;

Query Match 100.0%; Score 1276; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKRVLAFCFAALFSSQALALVATGNTTTKPDLYLYLKNSEAINSLALLPPPPAVGSI AF 60
 DB 1 MKKRVLAFCFAALFSSQALALVATGNTTTKPDLYLYLKNSEAINSLALLPPPPAVGSI AF 60
 QY 61 LNPQAMYEQGRLLRNTGRKLAEDANLSSGGVANAFSGAFSPITRKDAPALHKLITNM 120
 DB 61 LNPQAMYEQGRLLRNTGRKLAEDANLSSGGVANAFSGAFSPITRKDAPALHKLITNM 120
 QY 121 IEDAGDLATRSKADHYRIIRPFAYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
 DB 121 IEDAGDLATRSKADHYRIIRPFAYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
 QY 181 EINPQRONEILKRGYELGQSRVIGYHWSQSDVDARVVGSAVATLTNPAFQOOLQKAK 240
 DB 181 EINPQRONEILKRGYELGQSRVIGYHWSQSDVDARVVGSAVATLTNPAFQOOLQKAK 240
 QY 241 AEFAQHOKK 249
 DB 241 AEFAQHOKK 249

RESULT 3

AAW75064
 ID AAW75064 standard; protein; 249 AA.

AC AAW75064;

XX 23-JUL-2001 (first entry)

XX Escherichia blattae nucleotide-5'-phosphate producing enzyme protein.

XX Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;
 KW transphosphorylation; phosphatase; protein co-ordinate data;
 KW X-ray structural analysis; three-dimensional structure.

XX Escherichia blattae.

XX WC200118184-A1.

XX 15-MAR-2001.

XX 01-SEP-2000; 2000WO-JP005973.

XX 03-SEP-1999; 99JP-00249545.

XX (AJIN) AJINOMOTO CO INC.

XX Isikawa K, Suzuki E, Gondoh X, Shimba N, Mihara Y, Kawasaki H;

XX Kurahashi O, Kouda T, Shimacka M, Kozutsumi R, Asano Y;

XX WPI; 2001-380914/40.

XX N-PSDB; AAW19701.

PT Variant enzyme having elevated nucleoside 5'-prime phosphate producing
 PT activity and having a specific three-dimensional structure for production
 of nucleotides as pharmaceutical intermediates.

XX Disclosure; Page 157; 150pp; Japanese.

XX The present invention describes a variant nucleoside-5'-phosphate
 CC producing enzyme which is a modification of a transphosphorylase or
 CC phosphatase which contains a lysine, two arginine and two histidine
 CC residues and in which the C-alpha distances between these residues are
 CC enclosing a space which permits the binding of a nucleoside with these
 CC residues. Also described are: (1) a gene encoding the variant enzyme; (2)
 CC expression vectors containing the DNA; (3) host cells transformed by the
 CC vectors; (4) preparation of the variant enzyme by culture of the
 CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
 CC with molybdenic acid; and (6) selection of inhibitors of acid phosphatase
 CC or transphosphorylase using the structural coordinates derived from the
 CC enzyme. The variant enzymes with increased efficiency for production of
 CC nucleoside 5'-phosphates can be used as pharmaceutical intermediates.
 CC AAB19701 to AAB19785 and AAB75064 to AAB75101 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 249 AA;

Query Match 100.0%; Score 1276; DB 4; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKRVLCVFAALFSSQALALVATGNTTTTPDLYLKNSEAINSLALLPPPAVGSIAF 60
 Db |||||

Qy 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGVANAFSGAFSPITEKDAPALHKLNTNM 120
 Db |||||

Qy 121 IEDAGDLATRSADKHVMRIRPFYGVSTONTTQDKLSKNGSYPSGHTSIGWATALVLA 180
 Db |||||

Qy 181 EINPQRONEILKRGYELGOSRVICGYHWQSDVDAAARVGSVAVATLTNPAFOOQLOKAK 240
 Db |||||

Qy 241 AEPAQHOXK 249
 Db |||||

RESULT 4
 AAW71034
 ID AAW71034 standard; protein; 231 AA.

XX AAW71034;

XX 21-OCT-1998 (first entry)

XX Mutant acid phosphatase enzyme of Escherichia blattae.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 mutant; intermediate.

XX Synthetic.

XX Escherichia blattae.

XX Key Location/Qualifiers

XX Misc-difference 74

XX EP857788-A2.

XX 12-AUG-1998.

XX

PF 20-NOV-1997; 97EP-00309365.

XX 21-NOV-1996; 96JP-00311103.

XX 18-JUN-1997; 97JP-00161674.

XX (AJIN) AJINOMOTO CO INC.

XX Mihara Y, Utagawa T, Yamada H, Asano Y;

XX WPI; 1998-416010/36.

XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings
 or pharmaceutical intermediates.

XX Example 19; Page; 83pp; English.

XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
 CC created using the mature protein of AAW71029. The specification describes
 CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided

XX Sequence 231 AA;

Query Match 92.7%; Score 1183; DB 2; Length 231;
 Best Local Similarity 99.6%; Pred. No. 1.3e-118;
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSIAFNDQAMYEQGRLLNTER 78
 Db |||||

Qy 79 GKLAEDANLSSGVANAFSGAFSPITEKDAPALHKLNTNMIEDAGDLATRSADKHVMR 138
 Db |||||

Qy 139 IRPFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLAENPQRONEILKRGYELG 198
 Db |||||

Qy 199 QSRVICGYHWQSDVDAAARVGSVAVATLTNPAFOOQLOKAKAEPAQHOXK 249

Db 181 QSRVICGYHWQSDVDAAARVGSVAVATLTNPAFOOQLOKAKAEPAQHOXK 231

RESULT 5

AAW71035

XX AAW71035 standard; protein; 231 AA.

XX AAW71035;

XX 21-OCT-1998 (first entry)

XX Mutant acid phosphatase enzyme of Escherichia blattae.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 mutant; intermediate.

XX Synthetic.

XX Escherichia blattae.

XX Key Location/Qualifiers

XX Misc-difference 74

XX Misc-difference 153


```

FT XX EP857788-A2. /label= I153T
PN XX
XX XX
XX PD 12-AUG-1998.
XX XX
XX PF 20-NOV-1997; 97EP-00309365.
XX XX
XX PR 21-NOV-1996; 96JP-00311103.
XX PR 18-JUN-1997; 97JP-00161674.
XX XX
XX PA (AJIN ) AJINOMOTO CO INC.
XX XX
XX PI Mihara Y, Utagawa T, Yamada H, Asano Y;
XX XX WPI; 1998-416010/36.
XX XX
XX PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX PT with phosphate donor in presence of acid phosphatase - used as seasonings
XX PT or pharmaceutical intermediates.
XX XX
XX PS Example 13; Page; 83pp; English.
XX XX
XX CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX CC created using the mature protein of AAW71029. The specification describes
XX CC a method for the preparation of nucleoside 5'-phosphate esters. The
XX CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX CC 5.5 in the presence of an acid phosphatase that has been altered to
XX CC increase its affinity for the nucleoside and/or to increase its thermal
XX CC stability, or in the presence of a microorganism that has been
XX CC transformed with recombinant DNA containing a gene coding for such an
XX CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX CC pharmaceuticals or as intermediates for them. note: this sequence does
XX CC not appear in the specification; it was created using information
XX CC provided
XX XX
XX SQ Sequence 231 AA;
XX XX
XX Query Match 92.3%; Score 1178; DB 2; Length 231;
XX XX Best Local Similarity 99.18; Pred. No. 4.4e-118;
XX XX Matches 229; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX XX
QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPFLNDQAMYEQGLLRNTER 78
DB 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPFLNDQAMYEQGLLRNTER 60
QY 79 GKLAEDANLSSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGDLATRSKDHVYR 138
DB 61 GKLAEDANLSSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGDLATRSKDHVYR 120
QY 139 IRPFAFGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPNQNEILKRGYELG 198
DB 121 IRPFAFGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPNQNEILKRGYELG 180
QY 199 QSRVICGHWQSDVDAARVGSVAVVATLHTNPAFQQLOKAKAEFAQHKK 249
DB 181 QSRVICGHWQSDVDAARVGSVAVVATLHTNPAFQQLOKAKAEFAQHKK 231

RESULT 6
AAW71036
ID AAW71036 standard; protein; 231 AA.
XX XX
XX AC AAW71036;
XX XX
XX DT 21-OCT-1998 (first entry)
XX XX
XX DE Mutant acid phosphatase enzyme of Escherichia blattae.
XX XX
XX KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX KW mutant; intermediate.
XX OS Synthetic.

```

```

OS Escherichia blattae.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 63 /label= L63Q
XX FT Misc-difference 65 /label= A65Q
XX FT Misc-difference 66 /label= E66A
XX FT Misc-difference 74 /label= G74D
XX FT Misc-difference 153 /label= I153T
XX XX
XX PN EP857788-A2.
XX XX
XX PD 12-AUG-1998.
XX XX
XX PF 20-NOV-1997; 97EP-00309365.
XX XX
XX PR 21-NOV-1996; 96JP-00311103.
XX PR 18-JUN-1997; 97JP-00161674.
XX XX
XX PA (AJIN ) AJINOMOTO CO INC.
XX XX
XX PI Mihara Y, Utagawa T, Yamada H, Asano Y;
XX XX WPI; 1998-416010/36.
XX XX
XX PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX PT with phosphate donor in presence of acid phosphatase - used as seasonings
XX PT or pharmaceutical intermediates.
XX XX
XX PS Example 19; Page; 83pp; English.
XX XX
XX CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX CC created using the mature protein of AAW71029. The specification describes
XX CC a method for the preparation of nucleoside 5'-phosphate esters. The
XX CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX CC 5.5 in the presence of an acid phosphatase that has been altered to
XX CC increase its affinity for the nucleoside and/or to increase its thermal
XX CC stability, or in the presence of a microorganism that has been
XX CC transformed with recombinant DNA containing a gene coding for such an
XX CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX CC pharmaceuticals or as intermediates for them. note: this sequence does
XX CC not appear in the specification; it was created using information
XX CC provided
XX XX
XX SQ Sequence 231 AA;
XX XX
XX Query Match 91.04; Score 1161; DB 2; Length 231;
XX XX Best Local Similarity 97.84; Pred. No. 3e-116;
XX XX Matches 226; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX XX
QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPFLNDQAMYEQGLLRNTER 78
DB 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPFLNDQAMYEQGLLRNTER 60
QY 79 GKLAEDANLSSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGDLATRSKDHVYR 138
DB 61 GKLAEDANLSSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGDLATRSKDHVYR 120
QY 139 IRPFAFGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPNQNEILKRGYELG 196
DB 121 IRPFAFGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPNQNEILKRGYELG 180
QY 199 QSRVICGHWQSDVDAARVGSVAVVATLHTNPAFQQLOKAKAEFAQHKK 249
DB 181 QSRVICGHWQSDVDAARVGSVAVVATLHTNPAFQQLOKAKAEFAQHKK 231

RESULT 7
AAW06458

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ID XX AAW06458 standard; protein; 248 AA.
AC XX AAW06459;
DT DT 13-AUG-1997 (first entry)
DE DE Enterobacter aerogenes IFO 12010 acid phosphatase.
XX XX IFO 12010; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
KW KW condiment; pharmaceutical; intermediate.
XX XX Enterobacter aerogenes.
OS OS
FH FH Key Location/Qualifiers
FT FT Misc-difference 92 /note= "optionally replaced by another amino acid"
FT FT Misc-difference 171 /note= "optionally rep-aced by another amino acid"
XX XX
PN PN WO9637603-A1.
XX XX
PD PD 28-NOV-1996.
XX XX
PF PF 24-MAY-1996; 96WO-JP001402.
XX XX
PR PR 25-MAY-1995; 95JP-00149781.
PR PR 26-MAR-1996; 96JP-00094680.
XX XX
PA (AJIN) AJINOMOTO CO INC.
XX XX
PI PI Mihara Y, Utagawa T, Yamada H, Asano Y;
XX XX
DR DR WPI; 1997-021215/02.
DR DR N-PSDB; AAT45007.
XX XX
XX XX Efficient production of nucleoside 5'-phosphate - by reaction of a
PT PT nucleoside with a phosphoric acid donor in the presence of an acid
PT PT phosphatase.
XX XX
PS PS Claim 3; Page 67-68; 95pp; Japanese.
XX XX
CC CC The present sequence is the Enterobacter aerogenes IFO 12010 acid
CC CC phosphatase (API), which can be used to produce a nucleoside 5'-phosphate
CC CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
CC CC -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
CC CC 3.0 to 5.5. The PA can be used for the economic and efficient production
CC CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
CC CC and intermediates for pharmaceuticals
XX XX
SQ SQ Sequence 248 AA;

Query Match 90.8%; Score 1159; DB 2; Length 248;
Best Local Similarity 90.3%; Pred. No. 6.9e-116;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLCVCPAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVLCVCPAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60

QY 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGCVANAFSGAFSPITEKDAFALHKLITNM 120
DB 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGCVANAFSGAFSPITEKDAFALHKLITNM 120

QY 121 IEDAGDLATRSADHMYRIRPFAPYGVSTCNTTQDKLSKNGSPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSADHMYRIRPFAPYGVSTCNTTQDKLSKNGSPSGHTSIGWATALVLA 180

QY 181 EINFQRONEILKRGYELGQSVICGYHWQSDVDAARVVGSAVATLHTNPAFQOOLQKAK 240
DB 181 EINFQRONEILKRGYELGQSVICGYHWQSDVDAARVVGSAVATLHTNPAFQOOLQKAK 240

QY 241 AEFAQHOK 248
|||:

Db 241 DEFAKTQK 248

RESULT 8
AAW71031
ID AAW71031 standard; protein; 248 AA.
XX AC AAW71031;
XX AC AAW71031;
DT DT 21-OCT-1998 (first entry)
XX XX
DE DE Acid phosphatase enzyme amino acid sequence.
XX XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW KW intermediate.
XX XX Enterobacter aerogenes.
OS OS
XX XX BP857788-A2.
PN PN
PD PD 12-AUG-1998.
XX XX
PF PF 20-NOV-1997; 97EP-00309365.
XX XX
PR PR 21-NOV-1996; 96JP-00311103.
PR PR 18-JUN-1997; 97JP-00161674.
XX XX
PA (AJIN) AJINOMOTO CO INC.
XX XX
PI PI Mihara Y, Utagawa T, Yamada H, Asano Y;
XX XX
DR DR WPI; 1998-416010/36.
DR DR N-PSDB; AAV43060.
XX XX
XX XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT PT or pharmaceutical intermediates.
XX XX
PS PS Example 23; Page 44; 83pp; English.
XX XX
CC CC The present sequence represents an acid phosphatase enzyme. The
CC CC specification describes a method for the preparation of nucleoside 5'-
CC CC phosphate esters. The method comprises reacting a nucleoside with a
CC CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
CC CC has been altered to increase its affinity for the nucleoside and/or to
CC CC increase its thermal stability, or in the presence of a microorganism
CC CC that has been transformed with recombinant DNA containing a gene coding
CC CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
CC CC seasonings or pharmaceuticals or as intermediates for them
XX XX
SQ SQ Sequence 248 AA;

Query Match 90.8%; Score 1159; DB 2; Length 248;
Best Local Similarity 90.3%; Pred. No. 6.9e-116;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLCVCPAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVLCVCPAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60

QY 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGCVANAFSGAFSPITEKDAFALHKLITNM 120
DB 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGCVANAFSGAFSPITEKDAFALHKLITNM 120

QY 121 IEDAGDLATRSADHMYRIRPFAPYGVSTCNTTQDKLSKNGSPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSADHMYRIRPFAPYGVSTCNTTQDKLSKNGSPSGHTSIGWATALVLA 180

QY 181 EINFQRONEILKRGYELGQSVICGYHWQSDVDAARVVGSAVATLHTNPAFQOOLQKAK 240
DB 181 EINFQRONEILKRGYELGQSVICGYHWQSDVDAARVVGSAVATLHTNPAFQOOLQKAK 240

QY 241 AEFAQHOK 248

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Db.      241 DEFQKQK 248
||||: ||
RESULT 9
AAW71037
ID AAW71037 standard; protein; 231 AA.
XX
AC AAW71037;
XX
DT 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of Escherichia blattae.
XX
KW Acid phosphatase; preparation; nuc-eoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.
XX
OS Synthetic.
OS Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 63 /label= L63Q
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66 /label= E66A
FT Misc-difference 74 /label= G74D
FT Misc-difference 85 /label= S85Y
FT Misc-difference 153 /label= I153T
XX
DN EP857788-A2.
XX
PD 12-AUG-1998.
XX
PF 20-NOV-1997; 97EP-00309365.
XX
PR 21-NOV-1996; 96JP-00311103.
PR 18-JUN-1997; 97JP-00161674.
XX
PA (AJIN ) AJINOMOTO CO INC.
XX
PI Mihara Y, Utagawa T, Yamada H, Asano Y;
XX
DR WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
XX
PS Example 19; Page; 83pp; English.
XX
CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
SQ Sequence 231 AA;
Query Match 90.5%; Score 1155; DB 2; Length 231;
Best Local Similarity 97.4%; Pred. No. 1.3e-115;
Matches 225; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPNDQAMYQGRLLRNTER 78
|||
DB 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPNDQAMYQGRLLRNTER 60
|||
QY 79 GKLAEDANLSSGGVANAFSGAFGSPITEKDAHALHLLTNMIEDAGDLATRSKDHVYR 138
|||
DB 61 GKQAQADANLSSGGVANAFSGAFGSPITEKDAHALHLLTNMIEDAGDLATRSKDHVYR 120
|||
QY 139 IRPFAYGVSTCNTTEQDKLSKNGSYSGHTSIGWATLVIAEINPORQNEILKRGYELG 198
|||
DB 121 IRPFAYGVSTCNTTEQDKLSKNGSYSGHTSIGWATLVIAEINPORQNEILKRGYELG 180
|||
QY 199 QSRVICGYHQSDVDAARVVGSAVVATLHTNPAPQOOLQKAKAFPAHQKK 249
|||
DB 181 QSRVICGYHQSDVDAARVVGSAVVATLHTNPAPQOOLQKAKAFPAHQKK 231
|||
RESULT 10
AAW71038
ID AAW71038 standard; protein; 231 AA.
XX
AC AAW71038;
XX
DT 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of Escherichia blattae.
XX
KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.
XX
OS Synthetic.
OS Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 63 /label= L63Q
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66 /label= E66A
FT Misc-difference 74 /label= G74D
FT Misc-difference 135 /label= T135K
FT Misc-difference 136 /label= E136D
FT Misc-difference 153 /label= I153T
XX
XX EP857788-A2.
XX
FN 12-AUG-1998.
XX
PD 20-NOV-1997; 97EP-00309365.
XX
PF 21-NOV-1996; 96JP-00311103.
PR 18-JUN-1997; 97JP-00161674.
XX
PA (AJIN ) AJINOMOTO CO INC.
XX
PI Mihara Y, Utagawa T, Yamada H, Asano Y;
XX
DR WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
XX
PS Example 19; Page; 83pp; English.
XX
CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes

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CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
SQ Sequence 231 AA;
Query Match 90.3%; Score 1152; DB 2; Length 231;
Best Local Similarity 97.0%; Pred. No. 2.8e-115;
Matches 224; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 19 LALVATGNDTTTTPDLYLKNSAINSIALPPPPVAVGSIAPNDQAMYEQGRLLNTER 78
DB 1 LALVATGNDTTTTPDLYLKNSAINSIALPPPPVAVGSIAPNDQAMYEQGRLLNTER 60
QY 79 GKLAEDANLSSGVANAFSGARSPITEKDAPALHKLITNMIEDAGLATRSADHTMR 138
DB 61 GKQAQADANLSSGVANAFSGARSPITEKDAPALHKLITNMIEDAGLATRSADHTMR 120
QY 139 IRPFAEYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLAELNIPQONEILKRGYELG 198
DB 121 IRPFAEYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLAELNIPQONEILKRGYELG 180
QY 199 QSRVICYGHWQSDVDAARVGSVAVVATLHTNPFAFQQQLQKAKAEPAHQKK 249
DB 181 QSRVICYGHWQSDVDAARVGSVAVVATLHTNPFAFQQQLQKAKAEPAHQKK 231
RESULT 11
AAW06459
ID AAWC6459 standard; protein; 248 AA.
XX
AC AAW06459;
XX
DT 17-OCT-2003 (revised)
DT 13-AUG-1997 (first entry)
DE Klebsiella planticola IFO 14939 acid phosphatase.
XX
KW IFO 14939; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
KW condiment; pharmaceutical; intermediate.
XX
OS Racutella planticola.
XX
PH Key Location/Qualifiers
FT Misc-difference 92
FT Misc-difference /note= "optionally replaced by another amino acid"
FT Misc-difference 171
FT Misc-difference /note= "optionally replaced by another amino acid"
XX
EN WO9637603-A1.
XX
PD 28-NOV-1996.
XX
PF 24-MAY-1996; 96WO-JP001402.
XX
PR 25-MAY-1995; 95JP-00149781.
PR 26-MAR-1996; 96JP-00094680.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Mihara Y, Utagawa T, Yamada H, Asano Y;
XX
DR WPI; 1997-021215/22.
DR N-PSDB; AAY45C08.
XX
PT Efficient production of nucleoside 5'-phosphate - by reaction of a

PT nucleoside with a phosphoric acid donor in the presence of an acid
PT phosphatase.
XX
PS Claim 3; Page 70-72; 95pp; Japanese.
XX
CC The present sequence is the Klebsiella planticola IFO 14939 acid
CC phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
CC -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
CC 3.0 to 5.5. The PA can be used for the economic and efficient production
CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
CC and intermediates for pharmaceuticals. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 248 AA;
Query Match 89.6%; Score 1143; DB 2; Length 248;
Best Local Similarity 89.1%; Pred. No. 2.9e-114;
Matches 221; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
QY 1 MKKRVAVCFPAALFSSQALAVATGNDTTTTPDLYLKNSAINSIALPPPPVAVGSIAP 50
DB 1 MKKRVAVCFPAALFSSQALAVATGNDTTTTPDLYLKNSAINSIALPPPPVAVGSIAP 60
QY 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGVANAFSGARSPITEKDAPALHKLITNM 120
DB 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGVANAFSGARSPITEKDAPALHKLITNM 120
QY 121 IEDAGLATRSADHTMRIRPFAEYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGLATRSADHTMRIRPFAEYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLA 180
QY 181 EINPQONEILKRGYELGQSRVICGYHWSQSDVDAARVGSVAVVATLHTNPFAFQQQLQKAK 240
DB 181 EINPQONEILKRGYELGQSRVICGYHWSQSDVDAARVGSVAVVATLHTNPFAFQQQLQKAK 240
QY 241 AEPAHQKK 248
DB 241 DEFAHQKK 248
RESULT 12
AAW71032
ID AAW71032 standard; protein; 248 AA.
XX
AC AAW71032;
XX
DT 27-AUG-2003 (revised)
DT 21-OCT-1998 (first entry)
XX
DE Acid phosphatase enzyme amino acid sequence.
XX
KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW intermediate.
XX
OS Racutella planticola.
XX
PN EP857788-A2.
XX
PD 12-AUG-1998.
XX
PF 20-NOV-1997; 97EP-00309365.
XX
PR 21-NOV-1996; 96JP-00311103.
PR 18-JUN-1997; 97JP-00161674.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Mihara Y, Utagawa T, Yamada H, Asano Y;
XX
DR WPI; 1998-416010/36.
DR N-PSDB; AAV43061.
XX

PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.

XX Claim 6; Page 46-47; 83pp; English.

XX The present sequence represents an acid phosphatase enzyme. The
CC specification describes a method for the preparation of nucleoside 5'-
CC phosphate esters. The method comprises reacting a nucleoside with a
CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
CC has been altered to increase its affinity for the nucleoside and/or to
CC increase its thermal stability, or in the presence of a microorganism
CC that has been transformed with recombinant DNA containing a gene coding
CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
CC seasonings or pharmaceuticals or as intermediates for them. note: this
CC sequence appears as SEQ ID number 25 (nucleic acid) in the claims, but it
CC is clear that the protein is being claimed. (Updated on 27-AUG-2003 to
CC correct OS field.)

XX SQ Sequence 248 AA;

Query Match 89.6%; Score 1143; DB 2; Length 248;
Best Local Similarity 89.1%; Pred. No. 2.9e-114;
Matches 221; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 MKKRVLAVCFALFSSQALALVATGNDTTKPDLYLKNSEAINSLALLPPPPAVGSI 60
DB 1 MKKRVLALCLASFVSAPALVPAGNDATTKPDLYLKNQAIDSLALLPPPPVGVSI 60
QY 61 LNDQAMYEQGRLLNTERGKLAEDANLSGGVANAFSGAFSPITEKDAPALHKLITNM 120
DB 61 LNDQAMYEKGRLLNTERGKLAEDANLSAGGVANAFSAFSPITEKDAPALHKLITNM 120
QY 121 IEADGLATRSKDHVMRIIPFAFGVSTNTTEODKLSKNGSVPSGHTSIGWATLVLA 180
DB 121 IEADGLATRSKDHVMRIIPFAFGVSTNTTEODKLSKNGSVPSGHTSIGWATLVLA 180
QY 181 EINPQRCNEILKRGYELGQSRVIGYHWSQSDVDAAVVGSVAVATLHTNPAFQOOLQKAK 240
DB 181 EINPQRCNEILKRGYELGQSRVIGYHWSQSDVDAAVVGSVAVATLHTNPAFQOOLQKAK 240
QY 241 AEFAHQK 248
DB 241 DEFAQOK 248

RESULT 13
AAW71039
ID AAW71039 standard; protein; 231 AA.

XX AC AAW71039;

XX DT 21-OCT-1998 (first entry)

XX Mutant acid phosphatase enzyme of Escherichia blattae.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.

XX Synthetic.

OS Escherichia blattae.

XX Key Location/Qualifiers

FT Misc-difference 63 /label= L63Q

FT Misc-difference 65 /label= A65Q

FT Misc-difference 66 /label= E66A

FT Misc-difference 69 /label= N69D

FT Misc-difference 71 /label= S71A

FT Misc-difference 72 /label= S72A
FT Misc-difference 74 /label= G74D
FT Misc-difference 135 /label= T135K
FT Misc-difference 136 /label= E136D
FT Misc-difference 153 /label= I153T
XX

PN EP857788-A2.

XX 12-AUG-1998.

XX 20-NOV-1997; 97EP-00309365.

XX 21-NOV-1996; 96JP-00311103.

XX 18-JUN-1997; 97JP-00161674.

XX (AJIN) AJINOMOTO CO INC.

XX Mihara Y, Utagawa T, Yamada H, Asano Y;

XX WPI; 1998-416010/36.

XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.

XX Example 19; Page; 83pp; English.

XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided

XX SQ Sequence 231 AA;

Query Match 89.4%; Score 1141; DB 2; Length 231;
Best Local Similarity 95.7%; Pred. No. 4.2e-114;
Matches 221; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPLNDQAMYEQGRLLNTER 78
DB 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPLNDQAMYEQGRLLNTER 60
QY 79 GKLAEDANLSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGLATRSKDHVMR 138
DB 61 GKQAQADADLAAGDVANAFSGAFSPITEKDAPALHKLITNMIEDAGLATRSKDHVMR 120
QY 139 IRPFAFGVSTCNTTEODKLSKNGSVPSGHTSIGWATLVLAEPQNEILKRGYELG 198
DB 121 IRPFAFGVSTCNTTEODKLSKNGSVPSGHTSIGWATLVLAEPQNEILKRGYELG 180
QY 199 QSRVICGYHWSQSDVDAAVVGSVAVATLHTNPAFQOOLQKAKAEFAHQKX 249
DB 181 QSRVICGYHWSQSDVDAAVVGSVAVATLHTNPAFQOOLQKAKAEFAHQKX 231

RESULT 14

AAW71040

ID AAW71040 standard; protein; 231 AA.

XX AC AAW71040;

XX 21-OCT-1998 (first entry)
 XX Mutant acid phosphatase enzyme of Escherichia biattae.
 DE Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 XX mutant; intermediate.
 XX Synthetic.
 OS Escherichia biattae.
 XX Key Location/Qualifiers
 PH Misc-difference 63 /label= L63Q
 FT Misc-difference 65 /label= A65Q
 FT Misc-difference 66 /label= E66A
 FT Misc-difference 69 /label= M69D
 FT Misc-difference 71 /label= S71A
 FT Misc-difference 72 /label= S72A
 FT Misc-difference 74 /label= G74D
 FT Misc-difference 116 /label= D116E
 FT Misc-difference 135 /label= T135K
 FT Misc-difference 136 /label= E136D
 FT Misc-difference 153 /label= I153T
 XX EP857788-A2.
 PN 12-AUG-1998.
 XX 20-NOV-1997; 97EP-00309365.
 XX 21-NOV-1996; 96JP-00311103.
 XX 18-JUN-1997; 97JP-00161674.
 XX (AJIN) AJINOMOTO CO INC.
 XX Mihara Y, Utagawa T, Yamada H, Asano Y;
 PI MPI; 1998-416010/36.
 XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 XX with phosphate donor in presence of acid phosphatase - used as seasonings
 XX or pharmaceutical intermediates.
 XX Example 19; Page; 83pp; English.
 PS AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
 CC created using the mature protein of AAW71029. The specification describes
 CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided
 XX Sequence 231 AA;

Query Match 89.1%; Score 1137; DB 2; Length 231;
 Best Local Similarity 95.2%; Pred. No. 1.1e-113;

Matches 220; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 19 LALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSI AFLNDQAMYEQGRLLRNTER 78
 DB 1 LALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSI AFLNDQAMYEQGRLLRNTER 60
 QY 79 GKLAEDANLSSGGVANAFSGAFGSPITKDA PALHKLNTNMIEDAGDLATRSKDHYMR 138
 DB 61 GKQQAADADLAAGDVANAFSGAFGSPITKDA PALHKLNTNMIEDAGDLATRSKDHYMR 120
 QY 139 IRPFAYGVSTCNTKQDKLSKNGSYPSGHTSIGWATALVLAEPORONEILKRGVELG 198
 DB 121 IRPFAYGVSTCNTKQDKLSKNGSYPSGHTSIGWATALVLAEPORONEILKRGVELG 180
 QY 199 QSRVICGYHWCSDVDAARVVGVSAVATLHTNPAFQQOQLOKAKAEFAHQHX 249
 DB 181 QSRVICGYHWCSDVDAARVVGVSAVATLHTNPAFQQOQLOKAKAEFAHQHX 231
 RESULT 15
 AAW71041
 ID AAW71041 standard; protein; 231 AA.
 XX AAW71041;
 AC XX
 DT 21-OCT-1998 (first entry)
 XX Mutant acid phosphatase enzyme of Escherichia biattae.
 DE Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 XX mutant; intermediate.
 XX Synthetic.
 OS Escherichia biattae.
 XX Key Location/Qualifiers
 PH Misc-difference 63 /label= L63Q
 FT Misc-difference 65 /label= A65Q
 FT Misc-difference 66 /label= E66A
 FT Misc-difference 69 /label= M69D
 FT Misc-difference 71 /label= S71A
 FT Misc-difference 72 /label= S72A
 FT Misc-difference 74 /label= G74D
 FT Misc-difference 116 /label= D116E
 FT Misc-difference 130 /label= S130E
 FT Misc-difference 135 /label= T135K
 FT Misc-difference 136 /label= E136D
 FT Misc-difference 153 /label= I153T
 XX EP857788-A2.
 PN 12-AUG-1998.
 XX 20-NOV-1997; 97EP-00309365.
 XX 21-NOV-1996; 96JP-00311103.
 XX 18-JUN-1997; 97JP-00161674.
 XX (AJIN) AJINOMOTO CO INC.
 XX Mihara Y, Utagawa T, Yamada H, Asano Y;

Mon Jun 7 11:07:31 2004

XX WEI; 1998-416010/36.
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
XX
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
XX Sequence 231 AA;

Query Match 88.8%; Score 1133; DB 2; Length 231;
Best Local Similarity 94.8%; Pred. No. 3.1e-113;
Matches 219; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSGTAFLNDOAMYEQGRLLRNTER 78
DB 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSGTAFLNDOAMYEQGRLLRNTER 60
QY 79 GKLAEDANLSGGVANAFSGAFSPITEKAPALHKLNTNMIEDAGDLATRSKOHYMR 138
DB 61 GKQAQADADLAAGDVANAFSGAFSPITEKAPALHKLNTNMIEDAGDLATRSKOHYMR 120
QY 139 IRPPAFYGVSTCNTTQDKLSKNGSVPSGHTSIGWATLVLAIEINPQRQNEILKRGYELG 198
DB 121 IRPPAFYGVSTCNTQDKLSKNGSVPSGHTSIGWATLVLAIEINPQRQNEILKRGYELG 180
QY 199 QSRVICGHWQSDVDAARVVGSAVATLHTNPAPFOOLQKAKAEFAHQKK 249
DB 181 QSRVICGHWQSDVDAARVVGSAVATLHTNPAPFOOLQKAKAEFAHQKK 231

Search completed: June 2, 2004, 10:45:27
Job time : 63 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: June 2, 2004, 10:42:44 ; Search time 46 seconds
(without alignments)
1707.914 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKKRVLAVCPAALFSSQALA.....PAFOOQLOKAKFAHQKK 249

Scoring table: BLCSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315519202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.podent.*
- 12: sp.virus.*
- 13: sp.vertebrate.*
- 14: sp.unclassified.*
- 15: sp.rvirus.*
- 16: sp.bacteriap.*
- 17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1276	100.0	249	Q9SLA6	Q9SLA6 escherichia
2	1158	92.8	248	Q9FLU1	Q9FLU1 enterobacte
3	1143	89.6	248	Q9FLU0	Q9FLU0 klebsiella
4	1124	88.1	248	Q9RLW6	Q9RLW6 klebsiella
5	1048	82.1	249	Q50542	Q50542 shigella fl
6	1044	81.8	249	Q99Q99	Q99Q99 shigella fl
7	789	61.8	263	Q87188	Q87188 prevotella
8	596	46.7	246	Q99Q95	Q99Q95 shigella fl
9	591	46.3	246	Q99Q99	Q99Q99 shigella fl
10	590	46.2	246	Q931G8	Q931G8 escherichia
11	478	37.5	250	Q8KRUE	Q8KRUE salmonella
12	474.5	37.2	285	Q8PEI0	Q8PEI0 xanthomonas
13	433.5	34.0	280	Q8P342	Q8P342 xanthomonas
14	418.5	32.8	289	Q7TUQ8	Q7TUQ8 prochloroco
15	274.5	21.5	258	Q9AB73	Q9AB73 caulobacter
16	221	17.3	231	Q98HU7	Q98HU7 rhizobium 1

17	190	14.9	423	16	Q8ZLDS	Q8ZLDS salmonella
18	189.5	14.9	2314	16	Q69822	Q69822 streptomyce
19	175.5	13.8	241	16	Q916U4	Q916U4 pseudomonas
20	167	13.1	591	16	Q97L24	Q97L24 clostridium
21	149	11.7	986	16	Q87U02	Q87U02 pseudomonas
22	144.5	11.3	128	16	Q7TU07	Q7TU07 prochloroco
23	144.5	11.3	657	16	Q8Y350	Q8Y350 ralstonia s
24	143	11.2	622	16	Q8NR65	Q8NR65 corynebacte
25	141	11.1	660	16	Q8U788	Q8U788 agrobacteri
26	130.5	10.2	513	16	Q8G856	Q8G856 bifidobacte
27	115	9.0	260	16	Q8E929	Q8E929 shewanella
28	106.5	8.3	201	17	Q8TW45	Q8TW45 methanopyru
29	105	8.2	145	16	Q9RVL3	Q9RVL3 deinococcus
30	103.5	8.1	178	16	Q8R7A7	Q8R7A7 thermosarc
31	103	8.1	1381	17	Q8TRM0	Q8TRM0 methanosarc
32	101.5	8.0	266	16	Q89CT4	Q89CT4 bradyrhizob
33	100	7.8	230	16	Q9K3L3	Q9K3L3 streptomyce
34	99.5	7.8	151	16	Q8KFG2	Q8KFG2 chlorobium
35	99.5	7.8	259	16	Q9A424	Q9A424 caulobacter
36	99.5	7.8	353	10	Q84R60	Q84R60 oryza sativ
37	97.5	7.6	487	2	P72269	P72269 rhodococcus
38	96	7.5	178	16	Q9KP85	Q9KP85 vibrio chol
39	96	7.5	824	16	Q83SL8	Q83SL8 shigella fl
40	95.5	7.5	235	16	Q92KY7	Q92KY7 rhizobium m
41	95.5	7.5	307	16	Q8FLZ6	Q8FLZ6 corynebacte
42	95	7.4	320	16	Q8YWA0	Q8YWA0 anabaena sp
43	95	7.4	451	16	Q8G0H4	Q8G0H4 bruceella su
44	94	7.4	824	16	Q8X904	Q8X904 escherichia
45	94	7.4	1321	16	Q8PR59	Q8PR59 xanthomonas

ALIGNMENTS

RESULT 1

Q9SLA6 PRELIMINARY; PRT; 249 AA.
 AC Q9SLA6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Acid phosphatase (EC 3.1.3.2).
 GN PHO.
 OS Escherichia blattae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=563;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM1650;
 RX MEDLINE=20296667; PubMed=10835340;
 RA Ishikawa K., Mihara Y., Gondoh K., Suzuki E., Asano Y.;
 RT "X-ray structures of a novel acid phosphatase from Escherichia blattae
 RT and its complex with the transition-state analog molybdate.";
 RL EMBO J. 19:2412-2423 (2000).
 DR EMBL; AB020481; BAB84942.1; .
 DR PDB; 1D2T; 06-DEC-00.
 DR PDB; 1EO1; 23-MAR-01.
 DR PDB; 1TW8; 11-SEP-02.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR008934; AcPase VanPase.
 DR InterPro; IPR001011; Bac AcPaseA.
 DR InterPro; IPR000326; PA_PTPase.
 DR Pfam; PF01569; PAP2; 1.
 DR PRINTS; PR00483; BACPHTPASE.
 DR ProDom; PD009838; Bac AcPaseA; 1.
 DR SMART; SM00014; acidPPC; 1.
 DR PROSITE; PS01157; ACID_PHOSPH_CLA; 1.
 KW Hydrolase.
 SEQUENCE 249 AA; 26956 MW; 7AAE6CB61FC0CA3 CRC64;


```
Query Match 100.0%; Score 1276; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 4.8e-103;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKRVAVCFALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVAVCFALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSIAP 60

QY 61 LNDQMYEGRLRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
DB 61 LNDQMYEGRLRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120

QY 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180

QY 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFOOQLOKAK 240
DB 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFOOQLOKAK 240

QY 241 AEFQHQK 249
DB 241 AEFQHQK 249

RESULT 2
Q9F1U1 PRELIMINARY; PRT; 248 AA.
ID Q9F1U1
AC Q9F1U1
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Acid phosphatase.
GN PHO.
OS Klebsiella planticola (Raoultella planticola).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Raoultella.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO14939;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RT "Acid phosphatase/phosphotransferase from enteric bacteria.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044338; BAB1891.7; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000934; A:AcPase VanPerase.
DR InterPro; IPR001011; B:Ac AcPase.
DR InterPro; IPR00326; P:ATPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; B:Ac AcPaseA; 1.
DR SMART; SM00014; acdPPC; 1.
DR PROSITE; PS01157; ACID_PHOSP CL A; 1.
DR SEQUENCE 248 AA; 26963 MW; 208FAC2E5E862D CRC64;

Query Match 90.8%; Score 1158; DB 2; Length 248;
Best Local Similarity 90.3%; Pred. No. 9.1e-93;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVAVCFALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVAVCFALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSIAP 60

QY 61 LNDQMYEGRLRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
DB 61 LNDQMYEGRLRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120

QY 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180

QY 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFOOQLOKAK 240
DB 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFOOQLOKAK 240

QY 241 AEFQHQK 249
DB 241 AEFQHQK 249

RESULT 3
Q9F1U0 PRELIMINARY; PRT; 248 AA.
ID Q9F1U0
AC Q9F1U0
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Acid phosphatase.
GN PHO.
OS Klebsiella planticola (Raoultella planticola).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Raoultella.
OX NCBI_TaxID=575;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO14939;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RT "Acid phosphatase/phosphotransferase from enteric bacteria.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044345; BAB18918.1; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000934; A:AcPase VanPerase.
DR InterPro; IPR001011; B:Ac AcPase.
DR InterPro; IPR00326; P:ATPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; B:Ac AcPaseA; 1.
DR SMART; SM00014; acdPPC; 1.
DR PROSITE; PS01157; ACID_PHOSP CL A; 1.
DR SEQUENCE 248 AA; 26745 MW; 68F65CA2448EB3EF CRC64;

Query Match 89.6%; Score 1143; DB 2; Length 248;
Best Local Similarity 89.1%; Pred. No. 1.9e-91;
Matches 221; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 MKKRVAVCFALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVAVCFALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSIAP 60

QY 61 LNDQMYEGRLRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
DB 61 LNDQMYEGRLRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120

QY 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180

QY 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFOOQLOKAK 240
DB 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFOOQLOKAK 240

QY 241 AEFQHQK 248
DB 241 AEFQHQK 248

RESULT 4
Q9RLW6 PRELIMINARY; PRT; 248 AA.
ID Q9RLW6
AC Q9RLW6
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
```

DE Phoc protein precursor (EC 3.1.1.3.2).
GN PHOC.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]_SEQUENCE FROM N.A.
RP STRAIN=CCUG 225;
RC Passariello C., Berlutti F., Selan L., Thaller M.C., Rossolini G.;
RA "Klebsiella pneumoniae Phoc: a new member of the class A1 bacterial
RT acid phosphatases family";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250377; CAB59725.1; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR008934; ACPase VanPerase.
DR InterPro; IPR001011; Bac ACPaseA.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac ACPaseA; 1.
DR SMART; SM00014; acidPPC; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 248 PHOC.
SQ SEQUENCE 248 AA; 27110 MW; ED6E9D8663636B0D CRC64;

Query Match 88.1%; Score 1124; DB 2; Length 248;
Best Local Similarity 87.5%; Pred. No. 8.4e-90;
Matches 217; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKKRLVAVCFPAALFSSQALALVATGNDTTTKPDLYYLKNSAINSALLPPPPAVGSIAP 60
DB 1 MKKRLVAVCFPAALFSSQALALVATGNDTTTKPDLYYLKNSAINSALLPPPPAVGSIAP 60

QY 61 LNDQMYEQGRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAFALHKLNTNM 120
DB 61 LNDQMYEQGRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAFALHKLNTNM 120

QY 121 IEDAGDLATRSADHYMIRPFAPYGVSTCNTTQDKLKNGSPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSADHYMIRPFAPYGVSTCNTTQDKLKNGSPSGHTSIGWATALVLA 180

QY 181 EINPQRQNEILKRGYELGQSQSVICGYHWQSDVDAARVVGSAVATLTNPAFOOQLOKAK 240
DB 181 EINPQRQNEILKRGYELGQSQSVICGYHWQSDVDAARVVGSAVATLTNPAFOOQLOKAK 240

QY 241 AEFQHQK 248
DB 241 DEFQHQK 248

RESULT 5
ID OS0542 PRELIMINARY; PRT; 249 AA.
AC OS0542;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nonspecific phosphatase.
GN PHOC.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YSH6000;
RC MEDLINE=96345620; PubMed=8755883;
RX

RA Uchiya K., Toheuji M., Nikai T., Sugihara H., Sasaki C.;
RT "Identification and characterization of phoN-Sf, a gene on the large
RL plasmid of Shigella flexneri 2a encoding a nonspecific phosphatase";
RL J. Bacteriol. 178:4548-4554(1996).
DR EMBL; D82966; BA11655.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR008934; ACPase VanPerase.
DR InterPro; IPR001011; Bac ACPaseA.
DR InterPro; IPR000326; PA_PTPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac ACPaseA; 1.
DR SMART; SM00014; acidPPC; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
KW Plasmid.
SQ SEQUENCE 249 AA; 27177 MW; 58F34CEB034EE070 CRC64;

Query Match 82.1%; Score 1048; DB 2; Length 249;
Best Local Similarity 79.9%; Pred. No. 3.5e-83;
Matches 199; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

QY 1 MKKRLVAVCFPAALFSSQALALVATGNDTTTKPDLYYLKNSAINSALLPPPPAVGSIAP 60
DB 1 MKKRLVAVCFPAALFSSQALALVATGNDTTTKPDLYYLKNSAINSALLPPPPAVGSIAP 60

QY 61 LNDQMYEQGRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAFALHKLNTNM 120
DB 61 LNDQMYEQGRLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAFALHKLNTNM 120

QY 121 IEDAGDLATRSADHYMIRPFAPYGVSTCNTTQDKLKNGSPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSADHYMIRPFAPYGVSTCNTTQDKLKNGSPSGHTSIGWATALVLA 180

QY 181 EINPQRQNEILKRGYELGQSQSVICGYHWQSDVDAARVVGSAVATLTNPAFOOQLOKAK 240
DB 181 EINPQRQNEILKRGYELGQSQSVICGYHWQSDVDAARVVGSAVATLTNPAFOOQLOKAK 240

QY 241 AEFQHQK 249
DB 241 DEFQHQK 249

RESULT 6
ID Q99Q99 PRELIMINARY; PRT; 249 AA.
AC Q99Q99;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phon1, periplasmic non specific acid oisophatase (Phoshatase precursor)
GN PHON1 OR PHON-SF.
OS Shigella flexneri, and
OS Shigella flexneri 2a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623, 42897;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=M90T;
RC MEDLINE=20566792; PubMed=1115111;
RA Buchrieser C., Glaser P., Rusniok C., Nedjari H., d'Hauteville H.,
RA Kunst F., Sansonetti P., Parsot C.;
RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
RL by the type III secretion apparatus of Shigella flexneri";
RL Mol. Microbiol. 38:760-771(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; PLASMID=virulence pWR501;
RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,
RA Blattner F.R.;


```

RT Shigella flexneri.;
RL Infect. Immun. 0:0-0(2001).
DR EMBL; AL391753; CAC05771.1; -.
DR EMBL; AF348706; AAK18315.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR008934; AcPase VanPerase.
DR InterPro; IPR001011; Bac AcPataseA.
DR InterPro; IPR000326; PA_Ptase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPataseA; 1.
DR SMART; SM00014; acidPPC; 1.
KW Plasmid.
SQ SEQUENCE 246 AA; 27559 MW; 48D76BD8CC7885E5 CRC64;

Query Match 46.7%; Score 596; DB 2; Length 246;
Best Local Similarity 48.6%; Pred. No. 8.6e-44;
Matches 119; Conservative 44; Mismatches 69; Indels 14; Gaps 3;

QY 3 KRVLAVCFAA--LFSSQALALVATGNDTTTPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 4 KNFLFLCIATNMIFIPSANALKAEG-----FLTQQTSPDLSILPPPPAVNSVVF 53

QY 61 LNDQAMYEQGRLLRNTGRGKLAEDANILSSGGVANAFSGAFSPITEKDPALHKLITNM 120
DB 54 LADKAHYEFGSLRDANVRVLAEDAYYENFGL--AFSDAYGMDISRENTPIYQLITQV 111

QY 121 IEDAGDLATRSADHYMRIRPFAPYGVSTQNTTEODKLSKNGSPSGHTSIGWATALVIA 180
DB 112 LQSDHDAVRAKAYKVRPFVIYKDATCTPDKDKMAITGSPSGHAFGMAVALILA 171

QY 181 EINPQRONEILKRGVEYLGQSRIVCYHMQSDVDAAVVGSAAVATLHTNPAFOOQLOKAK 240
DB 172 EINPQRKAEILLRGGYEGESRIVCGAHWQSDVEAGRLMGASVVAVLHNTPEFTKSLSEAK 231

QY 241 AEPAQ 245
DB 232 KEFEE 236

RESULT 9
Q59909
ID Q59909 PRELIMINARY; PRT; 246 AA.
AC Q59909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATP diphosphohydrolase, apyrase precursor (BC 3.6.1.5).
GN Apy.
OS Shigella flexneri, and
OS Shigella flexneri 2a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
CX NCBI_TaxID=623, 42897;
[1]
RN SEQUENCE FROM N.A.
RP SPECIES=S.flexneri; STRAIN=2a;
RC Ramchandran V., Sankaran K., Subrahmanyam Y.V.B.K., Ramakrishnan R.,
RA Datta S., Roy R.K.;
RT "Virulent Shigella codes for a soluble apyrase : Identification,
RL characterisation and cloning of the gene.";
RN Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP SPECIES=S.flexneri 2a; STRAIN=301; PLASMID=PCP301;
RA Jin Q., Zhang J.Y., Liu H., Yang J., Yang F., Zhang X.B., Wang J.H.,
RA Yang G.W., Wu H.T., Dong J., Sun L.L., Xue Y., Zhao A.L., Gao Y.S.,
RA Zhu J.P., Kan B., Chen S.X., Yao Z.J., He B.K., Chen R.S., Ma D.L.,
RA Yuan Z.H., Xu J.G., Wang Y., Shen Y., Lu W.C., Qiang B.Q., Wen Y.M.,
RA Hou Y.D.;
RT "Complete DNA sequence and analysis of the large virulence plasmid

```

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RT pCP301 of Shigella flexneri.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04539; AAA21206.1; -.
DR EMBL; AF386526; AAL72358.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0004050; F:apyrase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR008934; AcPase VanPerase.
DR InterPro; IPR001011; Bac AcPataseA.
DR InterPro; IPR000326; PA_Ptase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPataseA; 1.
DR SMART; SM00014; acidPPC; 1.
KW Hydrolase; Signal; Plasmid.
FT SIGNAL 1 23
SQ SEQUENCE 246 AA; 27573 MW; B81737D9B6143912 CRC64;

Query Match 46.3%; Score 591; DB 2; Length 246;
Best Local Similarity 48.2%; Pred. No. 2.3e-43;
Matches 118; Conservative 44; Mismatches 69; Indels 14; Gaps 3;

QY 3 KRVLAVCFAA--LFSSQALALVATGNDTTTPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 4 KNFLFLCIATNMIFIPSANALKAEG-----FLTQQTSPDLSILPPPPAVNSVVF 53

QY 61 LNDQAMYEQGRLLRNTGRGKLAEDANILSSGGVANAFSGAFSPITEKDPALHKLITNM 120
DB 54 QADKAHYEFGSLRDANVRVLAEDAYYENFGL--AFSDAYGMDISRENTPIYQLITQV 111

QY 121 IEDAGDLATRSADHYMRIRPFAPYGVSTQNTTEODKLSKNGSPSGHTSIGWATALVIA 180
DB 112 LQSDHDAVRAKAYKVRPFVIYKDATCTPDKDKMAITGSPSGHAFGMAVALILA 171

QY 181 EINPQRONEILKRGVEYLGQSRIVCYHMQSDVDAAVVGSAAVATLHTNPAFOOQLOKAK 240
DB 172 EINPQRKAEILLRGGYEGESRIVCGAHWQSDVEAGRLMGASVVAVLHNTPEFTKSLSEAK 231

QY 241 AEPAQ 245
DB 232 KEFEE 236

RESULT 10
Q93IG8
ID Q93IG8 PRELIMINARY; PRT; 246 AA.
AC Q93IG8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Apyrase (BC 3.6.1.5).
GN Apy.
OS Escherichia coli.
OS Plasmid pHN280.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RP Santapaula D., Casalino M., Petrucci A., Presutti C., Zagaglia C.,
RA Berlutti F., Colonna B., Nicoletti M.;
RT "Virulence plasmid-carried apyrase gene (apy) is cotranscribed with the
RN upstream ospB gene in enteroinvasive Escherichia coli: study of
RT transcriptional organization and regulation of the ospB-apy operon.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ315184; CAC67470.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0004050; F:apyrase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.

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Query Match	37.5%	Score 478;	DB 2;	Length 250;
Best Local Similarity	47.0%	Pred. No. 1.7e-33;		
Matches	95;	Conservative	32;	Mismatches 75;
				Indels 0;
				Gaps 0;

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Qy 96 AFSGAFSPITEKDAPALHKLLTNMIEDAGLATRSKADHYMRIRPFAYGVSTCNTTQ 155
      : : : : :
Db 108 HFSICALGVQIDQATTPHLLRLLESLRDA-STSTSAAGRYQRPFFMNNQPMCTPAD 166
      : : : : :
Qy 156 DKLSKNGSYSPSGHTSIGWATLVLAETNPQRNQLKRGYELQGRVTCGYHWQSDVDA 215
      : : : : :
Db 167 DSLRKNGSYSPSGHTAIGWSWGLLAEALPARRDALLARGFRAGDSRLVCNVHWQSDVL 226
      : : : : :
Qy 216 RVVGSVAVTALHTNPAFQOQLOKAKAFQAQ 245
      : : : : :
Db 227 RIMGAAVVAALHGNAEFONDIAARRBIAK 256
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RESULT 14
Q7TU08
ID Q7TU08 PRELIMINARY; ERT; 289 AA.
AC Q7TU08;
DT 01-OCT-2003 {TrEMBLrel. 25, Created}
DT 01-OCT-2003 {TrEMBLrel. 25, Last sequence update}
DT 01-OCT-2003 {TrEMBLrel. 25, Last annotation update}
DE PA-phosphatase related phosphoesterase:bacterial acid phosphatase. . .
DE precursor {EC 3.1.3.2}.
GN PHON OR PWT1569.
OS Prochlorococcus marinus (strain MIT 9313) .
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
CC NCBI_TaxID=74547;
CX [1]
RN
RP
RX SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642;
RA Recap G., Larimer F.W., Lamedin J., Malfatti S., Chain P.,
RA Allgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,

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Db 249 ADFFSDFAAAAEVSEARSR 258

RESULT 15

Q9AB73

ID Q9AB73 PRELIMINARY; PRT; 258 AA.

AC Q9AB73;

DT 01-JUN-2001 (TReMBLrel. 17, Created)
BT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Acid phosphatase.
GN CC0358.
CS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
CX NCBI_TaxID=155892;
RN [-]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C.; Feldblyum T.V.; Laub M.T.; Paulsen I.T.; Nelson K.E.;
RA Eisen J.; Heidelberg J.F.; Alley M.R.K.; Ohta N.; Maddock J.R.; Ely B.;
RA Potocka I.; Nelson W.C.; Newton A.; Stephens C.; Shadke N.B.; Ely B.;
RA DeBey R.T.; Dodson R.J.; Durkin A.S.; Gwinn M.L.; Haft D.H.;
RA Kolonay J.F.; Smit J.; Craven M.B.; Khouri H.; Shetty J.; Berry K.;
RA Uterback T.; Tran K.; Wolf A.; Vamathevan J.; Ermolaeva M.; White O.;
RA Salzberg S.L.; Venter J.C.; Shapiro L.; Fraser C.M.;
RT *Complete genome sequence of Caulobacter crescentus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005709; AAK22345.1; -.
DR PIR; E87293; E87293.
DR TIGR; CC0358; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR008934; AcPase_VanPerase.
DR InterPro; IPR001011; Bac_AcPaseA.
DR InterPro; IPR000326; PA_PTPase.
DR InterPro; IPR000437; Prok_lipoprot_S.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODOM; PD009838; Bac_AcPaseA; 1.
DR SMART; SM00014; acidPPC; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 27634 MW; AAA962EF79AB9543 CRC64;

Query Match 21.5%; Score 274.5; DB 16; Length 258;
Best Local Similarity 34.6%; Pred. No. 9.fe-16;
Matches 80; Conservative 35; Mismatches 109; Indels 7; Gaps 7;

QY 13 LFSQALALVATGNDTWTTPDYLYLKNSEAINSLALLPPPPAVGSIAPLNDQAMYEQRL 72
DB 6 LVTTAALMLTGCATLSGDAENRYLAGK-VFDADHLPPPPAKGSEALRDREIFRATRA 64

QY 73 LRNTERGKLAEDANLSSGGVANAFSGAFG-SPITEKDAPALEKLLTNMIEDAGDLATRS 131
DB 65 LKDTPRWSLAQED-NVEE-KYLOGYACALGVTPSFERN-PKLAIVTLRLMSRDVRS-AVAG 120

QY 132 AKDHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWTALVLAEINPORNEIL 191
DB 121 PKLYRPRPFYFSEEGPIC-IKRLGLALSDFYPSGHTWGSVGLVLAEVAPDRRAIL 179

QY 192 KRGVELQGSRVICGYHMQSDYDAARVVGSAVVATLHTNPAPQOOLQAKAE 242
DB 180 ARAQAYGESRVVCGVHNSSVEAGRMNAEKLLSALKSSDAFKADLAARAE 230

Search completed: June 2, 2004, 10:46:58
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

QM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 17:54:16 ; Search time 3428 Seconds
(without alignments)
15498.686 Million cell updates/sec

Title: US-09-807-990-1

Perfect score: 1225

Sequence: 1 ctcgacgcgaaggaagcgtg.....taagatcatgtgcggttaac 1225

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:*

2: gb_hg:*

3: gb_in:*

4: gb_ov:*

5: gb_ov:*

6: gb_pat:*

7: gb_pl:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_or:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pi:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

42: em_htgo_mus:*

43: em_htgo_mus:*

44: em_htgo_mus:*

45: em_htgo_mus:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1225	100.0	1225	1	AB020481	AB020481 Escherich
2	1225	100.0	1225	6	BD014522	BD014522 Variant n
3	1225	100.0	1225	6	BD093734	BD093734 Variant n
4	750	61.2	750	6	AR140145	AR140145 Sequence
5	750	61.2	750	6	E16585	E16585 Escherichia
6	750	61.2	750	6	AR199634	AR199634 Sequence
7	750	61.2	750	6	BD017670	BD017670 Mutant ac
8	747	61.0	747	6	E12610	E12610 DNA encodin
9	514.6	42.0	762	6	AR384033	AR384033 Sequence
10	512.2	41.8	1650	1	AB044338	AB044338 Enterobac
11	507	41.4	747	6	AR140159	AR140159 Sequence
12	507	41.4	747	6	E16587	E16587 Enterobacte
13	507	41.4	747	6	AR199648	AR199648 Sequence
14	507	41.4	747	6	BD017677	BD017677 Mutant ac
15	502.2	41.0	2198	1	AB044345	AB044345 Klebsiell
16	501.8	41.0	1322	1	KPN250377	KPN250377 Klebsiell
17	494.6	40.4	1650	6	BD014526	BD014526 Variant n
18	494.6	40.4	1650	6	BD093738	BD093738 Variant n
19	493.4	40.3	747	6	AR140160	AR140160 Sequence
20	493.4	40.3	747	6	E16588	E16588 Klebsiella
21	493.4	40.3	747	6	AR199649	AR199649 Sequence
22	493.4	40.3	747	6	BD017678	BD017678 Mutant ac
23	423.6	34.6	1344	1	AB035805	AB035805 Morganell
24	423.6	34.6	1344	6	BD014523	BD014523 Variant n
25	423.6	34.6	1344	6	BD093735	BD093735 Variant n
26	422.4	34.5	1144	1	MMPHOC	X64444 M.morganii
27	422	34.4	750	6	AR140144	AR140144 Sequence
28	422	34.4	750	6	E16584	E16584 Morganella
29	422	34.4	750	6	AR199633	AR199633 Sequence
30	422	34.4	750	6	BD017666	BD017666 Mutant ac
31	419	34.2	747	6	E12606	E12606 DNA encodin
32	411.4	33.6	3626	12	ASPGREEN1	Y09373 Artificial
33	404.6	33.0	213494	1	SPFMR100	AL391753 Shigella
34	404.6	33.0	221618	1	AF386526	AF386526 Shigella
35	404.6	33.0	221851	1	AF348706	AF348706 Shigella
36	401.6	32.8	3633	12	ASPGREEN2	Y09374 Artificial
37	398	32.5	750	1	D82966	D82966 Shigella fl
38	360.2	29.4	1036	1	PSPHONG	X64820 P.stuartii
39	357.4	29.2	747	6	AR140158	AR140158 Sequence
40	357.4	29.2	747	6	E16586	E16586 Providencia
41	357.4	29.2	747	6	AR199647	AR199647 Sequence
42	357.4	29.2	747	6	BD017676	BD017676 Mutant ac
43	304.6	24.9	735	6	AR140161	AR140161 Sequence
44	304.6	24.9	735	6	E16589	E16589 Serratia fl
45	304.6	24.9	735	6	AR199650	AR199650 Sequence

ALIGNMENTS

RESULT 1
AB020481
LOCUS AB020481 Escherichia blattae gene for acid phosphatase, complete cds. 1225 bp DNA linear BCF 20-JUN-2000
DEFINITION Escherichia blattae gene for acid phosphatase, complete cds.
ACCESSION AB020481
VERSION AB020481.1 GI:6003516
KEYWORDS acid phosphatase.
SOURCE Escherichia blattae
ORGANISM Escherichia blattae
REFERENCE 1 (sites)
AUTHORS Ishikawa,K., Mihara,Y., Gondoh,K., Suzuki,E. and Asano,Y.
TITLE X-ray structures of a novel acid phosphatase from Escherichia blattae and its complex with the transition-state analog mo-ybdate

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

EMBO J. 19 (11), 2412-2423 (2000)
20296667
10835340
2 (bases 1 to 1225)
Mihara,Y. and Asano,Y.
Direct Submision
Submitted (25-NOV-1998) Yasuhiro Mihara, Ajinomoto Co., Inc.,
Fermentation and Biotechnology Laboratory, Kawasaki-ku, Suzuki-cho,
1-1, Kawasaki-shi, Kanagawa 210-8681, Japan
(E-mail:blid.mihara@ajinomoto.co.jp, Tel:81-44-244-7138,
Fax:81-44-244-4757)

FEATURES

Location/Qualifiers

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/organism="Escherichia blattae"

/mol_type="genomic DNA"

/strain="JCM1650"

/db_xref="taxon:563"

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/gene="pho"

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/gene="pho"

/EC number="3.1.3.2"

/codon_start=1

/transl_table=11

/product="acid phosphatase"

/protein_id="BA84942.1"

/db_xref="GI:6039517"

/translation="MKRVLAIVFAALFSSQALALVATGNDTTTKPOLYLYKNSALN
SLALLPPPAVGSIAFLINDQAMTEYQGLLRNTERGLAABDANLSSGVANAFSGAG
SPITEKDALPHKLILNMDIADGLATRSANDHYMRIRPFAYGVSTVTEQDKLSK
NGSVPSGHTSIGWATLVLAIRINPORONEILKRGVE-GQSRVIGYHWQSDVDAARVV
GSAVATLHTNPAPQQLQKAKAFHQKK"

ORIGIN

Query Match 100.0%; Score 1225; DB 1; Length 1225;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACGGGAAAGCAATGTGTGTCGGCGGTGAGCGGCACCTCTACGAGATTAAAGATAAG 60
DB 1 CTGACGGGAAAGCAATGTGTGTCGGCGGTGAGCGGCACCTCTACGAGATTAAAGATAAG 60

61 TAATATCCATTATACAGGTAACAGCAATGCTCTGAGTGTGATGTATACCTGAGCGG 120
DB 61 TAATATCCATTATACAGGTAACAGCAATGCTCTGAGTGTGATGTATACCTGAGCGG 120

121 CGCGGGGGTTCCTCCCGGCGGCTTTTATATGAGGCTCGCGTGGAGCGGTTATCTGCTG 180
DB 121 CGCGGGGGTTCCTCCCGGCGGCTTTTATATGAGGCTCGCGTGGAGCGGTTATCTGCTG 180

181 GCCCTGTTGTGCACAAACGCTTTATATGTAATTTTGTGCGTATATCAGGTTTTT 240
DB 181 GCCCTGTTGTGCACAAACGCTTTATATGTAATTTTGTGCGTATATCAGGTTTTT 240

241 AAGCACCTGTGGGCTCATACTGCAACCTGTTGATATTAAGCAACACTCTTCACTCAC 300
DB 241 AAGCACCTGTGGGCTCATACTGCAACCTGTTGATATTAAGCAACACTCTTCACTCAC 300

301 GGAATTAACACGACAGTAAGGTAATACGATGAAGAAAACGTTTCTGGCGTTGTTTT 360
DB 301 GGAATTAACACGACAGTAAGGTAATACGATGAAGAAAACGTTTCTGGCGTTGTTTT 360

361 GCCCATTTGTTCTCTTCAGGCCCTCGGCTGTCGCTACCGGCAAGCAGACTACACG 420
DB 361 GCCCATTTGTTCTCTTCAGGCCCTCGGCTGTCGCTACCGGCAAGCAGACTACACG 420

421 AAACCGGATCTCTACTACTCAAGAACAGTAGAGCCATTAAACAGCTGCGCTGTGCGG 480
DB 421 AAACCGGATCTCTACTACTCAAGAACAGTAGAGCCATTAAACAGCTGCGCTGTGCGG 480

481 CCACACCGGGGTGGGCTCCATGCGTTTCTCAAGCATCAGGCCATGTATGAACAGGGG 540
DB 481 CCACACCGGGGTGGGCTCCATGCGTTTCTCAAGCATCAGGCCATGTATGAACAGGGG 540

QY 541 CGCTCTGCTGGCAACACCGAACCGGTAAAGCTGGCGGCGGAAGATGCAAACTCAGCAGT 600
DB 541 CGCTCTGCTGGCAACACCGAACCGGTAAAGCTGGCGGCGGAAGATGCAAACTCAGCAGT 600

601 GCGGGGGTGCAGAAATGCTTTCTCGGCGCGTGTGGTAGCCGATCACCAGAAAGAGCGCC 660
DB 601 GCGGGGGTGCAGAAATGCTTTCTCGGCGCGTGTGGTAGCCGATCACCAGAAAGAGCGCC 660

661 CCGGCGCTGCATTAATTAATCTGACCAATATGATGAGCAGCGCGGATCTGCGCACCGC 720
DB 661 CCGGCGCTGCATTAATTAATCTGACCAATATGATGAGCAGCGCGGATCTGCGCACCGC 720

721 AGCGCGAAAGATCACTATATGCGCAATTCGTCGGTTTCGGTTTATGGGGTCTCTACCTGT 780
DB 721 AGCGCGAAAGATCACTATATGCGCAATTCGTCGGTTTCGGTTTATGGGGTCTCTACCTGT 780

781 AATACCAACGAGCAGGACAACTGTGTCAAAATGGCTCTTATCCGTGGGCGCATACCTCT 840
DB 781 AATACCAACGAGCAGGACAACTGTGTCAAAATGGCTCTTATCCGTGGGCGCATACCTCT 840

841 ATCGGCTGGGCTACTCGCTGGTGTGCTGCGCAGAGATCAACCTCAGCGCAGACGAGATC 900
DB 841 ATCGGCTGGGCTACTCGCTGGTGTGCTGCGCAGAGATCAACCTCAGCGCAGACGAGATC 900

901 CTGAAACCGCGGTTATGAGCTGGGCGCAGAGCGGGTGATTTGCGGCTACCACTGGCAGGT 960
DB 901 CTGAAACCGCGGTTATGAGCTGGGCGCAGAGCGGGTGATTTGCGGCTACCACTGGCAGGT 960

961 GATGTGATGCGCGCGGGTGTGAGTCTGCGCTGTGGCGACCTGTCATACCAACCGG 1020
DB 961 GATGTGATGCGCGCGGGTGTGAGTCTGCGCTGTGGCGACCTGTCATACCAACCGG 1020

1021 GCGTTCCAGCAGCAGTTGTCAGAAAGCGAAGCCGAATTCGCGCCAGCATCAGAAAGATAA 1080
DB 1021 GCGTTCCAGCAGCAGTTGTCAGAAAGCGAAGCCGAATTCGCGCCAGCATCAGAAAGATAA 1080

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DB 1141 TCCACAGTATATGACGGTATATGATTTGTGCAAGAAAGGTTGTTGTCACGCCACA 1200

1201 GCTATAGATCATGTGCGGTTAAC 1225
DB 1201 GCTATAGATCATGTGCGGTTAAC 1225

RESULT 2

BD014522

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD014522 1225 bp DNA linear PAT 27-AUG-2002
Variant nucleoside 5'-phosphate producing enzyme.

BD014522

BD014522.1 GI:22555305

JP 2001136984-A/1.

Escherichia blattae

Escherichia blattae

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Escherichia.

1 (bases 1 to 1225)

Ishikawa,K., Suzuki,E., Gondo,K., Shima,N., Mihara,Y., Kawasaki,H.,

Kurahashi,O., Koda,T., Shimaoka,M., Kozutsumi,R. and Asano,Y.

Variant nucleoside 5'-phosphate producing enzyme

Patent: JP 2001136984-A 1 22-MAY-2001;

AJINOMOTO CO INC

OS Escherichia blattae

PN JP 2001136984-A/1

PD 22-MAY-2001

PF 31-AUG-2000 JP 2000262120

PI KOKI ISHIKAWA, EIICHIRO SUZUKI, KEIKO GONDO, NOBUHISA SHIMBA, PI

YASUHIRO MIHARA,

```
PI HISASHI KAWASAKI, OSAMU KURAHASHI, TORU KODA, MEGUMI SHIMAOKA, RIE
PI KOZUTSUMI,
PI YASUHIISA ASANO
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/12, C12N9/
PC 16,
PC C12P19/38/(C12N15/09, C12R1:01), (C12N15/09, C12R1:185) PC
, (C12N15/09, C12R1:22),
PC (C12P19/38, C12R1:19), C12N15/00, C12N5/00, (C12N15/00, C12R1:01),
PC (C12N15/00, C12R1:185), (C12N15/00, C12R1:22)
CC Variant nucleoside 5'-phosphate producing enzyme FH Key
Location/Qualifiers
FT CDS (331)..(1077).
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 CGCGGGGTTCCCGGGCGCTTTTATGGGCTCGCGTGGAGCGCTTATCTGCTG 180
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QY 181 GCCCTGTTTGTGCACAAACGCTTTATGTGTAATTTTGTGAGTATACAGTGT 240
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DB 241 AAGCACCTGTGGGCTCTACTGCAACCTGTGATATTAGGCAACACTCTTCACTAC 300
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LOCUS Variant nucleoside-5'-phosphate producing enzyme.
DEFINITION BD093734
ACCESSION BD093734
VERSION BD093734.1 GI:22639322
KEYWORDS WO 0118184-A/1.
SOURCE unidentifed
ORGANISM unidentifed
REFERENCE 1. bases 1 to 1225)
AUTHORS Ishikawa, K., Suzuki, E., Gondo, K., Shimba, N., Wihar, Y., Kawasaki, H.,
Kurahashi, O., Koda, T., Shimaoka, M., Kozutsumi, R. and Asano, Y.
TITLE Variant nucleoside-5'-phosphate producing enzyme
JOURNAL Patent: WO 0118184-A 1 15-MAR-2001;
AJINOMOTO CO INC, KOKI ISHIKAWA, EIICHIRO SUZUKI, KEIKO GONDO, NOBUHISA
SHIMBA, YASUHIRO MIHARA, HISASHI KAWASAKI, OSAMU KURAHASHI, TORU
KODA, MEGUMI SHIMAOKA, RIE KOZUTSUMI, YASUHIISA ASANO
COMMENT OS Escherichia blattae
PN WO 0118184-A/1
PD 15-MAR-2001
PF 01-SEP-2000 WO 2000JP005973
PR 03-SEP-1999 JP 99P 249545
PI KOKI ISHIKAWA, EIICHIRO SUZUKI, KEIKO GONDO, NOBUHISA SHIMBA, PI
YASUHIRO MIHARA,
PI HISASHI KAWASAKI, OSAMU KURAHASHI, TORU KODA, MEGUMI SHIMAOKA, RIE
PI KOZUTSUMI,
PI YASUHIISA ASANO
PC C12N9/12, C12N15/54, C12N1/21/(C12N1/21, C12R1:19) CC
FH Key Location/Qualifiers
FT CDS (331)..(1077).
FEATURES
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Query Match 100.0%; Score 1225; DB 6; Length 1225;
 Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
 Matches 1225; Conservative 0; Mismatches 0

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ORIGIN

Query Match 61.2%; Score 750; DB 6; Length 750;
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 751 CGGTTCCGCTTTTATGGGCTCTTACTGTATAACCGGAGCGGAGCAAACTGCTCAAA 810
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ORIGIN

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 Matches 750; Conservative 0; Mismatches 0

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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 6.9e-198; Indels 0; Gaps 0;
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 61 CTGCT 120
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QY	811	ATGCGCTCTATCCGTCGGGATACCTCTATCGGCTGGGCTACGCGTGGTCTGGCA	870
DB	481	ATGCGCTCTATCCGTCGGGATACCTCTATCGGCTGGGCTACGCGTGGTCTGGCA	540
QY	871	GAGATCAACCTCAGCGCCAGAACGAGATCTTGAACGCGGTATGAGCTGGGCCAGAGC	930
DB	541	GAGATCAACCTCAGCGCCAGAACGAGATCTTGAACGCGGTATGAGCTGGGCCAGAGC	600
QY	931	CGGCTGATTTGGGCTACCACTGGCAGAGTGTGATGCGCGGGTGGTGGATCT	990
DB	601	CGGCTGATTTGGGCTACCACTGGCAGAGTGTGATGCGCGGGTGGTGGATCT	650
QY	991	GCGGTTGTGGCGACCTTGATACCAACCGCGGCTCCAGAGCAATGGCAAGCGAAG	1050
DB	651	GCGGTTGTGGCGACCTTGATACCAACCGCGGCTCCAGAGCAATGGCAAGCGAAG	720
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DB	721	GCGGAATTCGCCAGCATCAGAAATAA	750
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ACCESSION	E16585		
VERSION	E16585.1	GI:5711268	
KEYWORDS	JP 1998201481-A/2.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 750)		
AUTHORS	Mihara Y., Udagawa T., Yamada H. and Asano Y.		
TITLE	PRODUCTION OF NUCLEOSIDE 5'-PHOSPHATE		
JOURNAL	Patent: JP 199820148-A 2 04-AUG-1998;		
COMMENT	AJINOMOTO CO INC		
	OS Escherichia blattae		
	PN JP 1998201481-A/2		
	PD 04-AUG-1998		
	PF 18-JUN-1997 JP 1997161674		
	PR 21-NOV-1996 JP 96P 311103		
	PI MIHARA YASUHIRO, UDAGAWA TAKASHI, YAMADA HIDEAKI, PI ASANO		
	YASUHIRO		
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	CC topology: Linear;		
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Matches 750;	Conservative 0;	Mismatches 0;	Gaps 0;
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DB	61	CTGGTGGCTACCGGAAACGACACTACCAAGAACCGGATCTCTACTACCTCAAGACAGT	120
QY	451	GAAGCAATTAAACAGCCTGGGCTGTTGGCCACCAACCGGCGGTGGCTCCATTCGCTTT	510
DB	121	GAAGCAATTAAACAGCCTGGGCTGTTGGCCACCAACCGGCGGTGGCTCCATTCGCTTT	180
QY	511	CTCAACGATCAGGCCATGTATGAACAGGGGCGCTGTGGCAACACCGAAGCGGTTAAG	570
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QY	571	CTGGCGCGAAGATGCAAACTGAGCAAGTGGCGGTGGCGAATGCTTTCTCGGCGCG	630
DB	241	CTGGCGCGAAGATGCAAACTGAGCAAGTGGCGGTGGCGAATGCTTTCTCGGCGCG	300
QY	631	TTTGGTAGCCCGATCACCGAAAAAGACGCCCGCGGCTGCATAAATTACTGACCAATATG	690
DB	301	TTTGGTAGCCCGATCACCGAAAAAGACGCCCGCGGCTGCATAAATTACTGACCAATATG	360
QY	691	ATTGAGGACGCGGGGATCTGGCGACCGCGGCGGATCTGCTATATATGCGCATTCGT	750
DB	361	ATTGAGGACGCGGGGATCTGGCGACCGCGGCGGATCTGCTATATATGCGCATTCGT	420
QY	751	CGGTGGCTTTATGGGCTCTACTCTGTAATACCGAGCAGCAAACTGTCCTAAA	810
DB	421	CGGTGGCTTTATGGGCTCTACTCTGTAATACCGAGCAGCAAACTGTCCTAAA	480
QY	811	ATGGCTCTTATCCGTCGGGATACCTCTATCGGCTGGGCTACGCGTGGTCTGGCA	870
DB	481	ATGGCTCTTATCCGTCGGGATACCTCTATCGGCTGGGCTACGCGTGGTCTGGCA	540
QY	871	GAGATCAACCTCAGCGCCAGAACGAGATCTTGAACGCGGTATGAGCTGGGCCAGAGC	930
DB	541	GAGATCAACCTCAGCGCCAGAACGAGATCTTGAACGCGGTATGAGCTGGGCCAGAGC	600
QY	931	CGGCTGATTTGGGCTACCACTGGCAGAGTGTGATGCGCGGGTGGTGGATCT	990
DB	601	CGGCTGATTTGGGCTACCACTGGCAGAGTGTGATGCGCGGGTGGTGGATCT	660
QY	991	GCGGTTGTGGCGACCTTGATACCAACCGCGGCTCCAGAGCAATGGCAAGCGAAG	1050
DB	661	GCGGTTGTGGCGACCTTGATACCAACCGCGGCTCCAGAGCAATGGCAAGCGAAG	720
QY	1051	GCGGAATTCGCCAGCATCAGAAATAA	1080
DB	721	GCGGAATTCGCCAGCATCAGAAATAA	750
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DEFINITION	Sequence 6 from patent US 6355472.		linear
ACCESSION	AR199634		
VERSION	AR199634.1	GI:20249708	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 750)		
AUTHORS	Mihara Y., Udagawa T., Yamada H. and Asano Y.		
TITLE	Method for producing nucleoside-5'-phosphate ester		
JOURNAL	Patent: US 6355472-A 6 12-MAR-2002;		
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source	1..750	/organism='unassigned DNA'	
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Query Match	61.2%;	Score 750;	DB 6; Length 750;
Best Local Similarity	100.0%;	Pred. No. 6.9e-198;	Indels 0;
Matches 750;	Conservative 0;	Mismatches 0;	Gaps 0;
QY	331	ATGAAAAACGTTCTGGCAGTTGTTTGGCGGATTTCTCTCTCAGCGCCCTGGCG	390
DB	1	ATGAAAAACGTTCTGGCAGTTGTTTGGCGGATTTCTCTCTCAGCGCCCTGGCG	60

[illegible]


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RESULT 8
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LOCUS      E12610
DEFINITION DNA encoding wild type acid phosphatase from Escherichia blattae.
ACCESSION E12610
VERSION    E12610.1
KEYWORDS   JP 1997037785-A/5.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 747)
AUTHORS    Mihara,Y., Udagawa,T., Yamada,H. and Asano,Y.
TITLE      PRODUCTION OF NUCLEOSIDE-5'-PHOSPHATE
JOURNAL    Patent: JP 1997037785-A 5 10-FEB-1997;
            AJINOMOTO CO INC
COMMENT    OS Escherichia blattae
            EN JP 1997037785-A/5
            ED 10-FEB-1997
            PF 26-MAR-1996 JP 1996094680
            PR 25-MAY-1995 JP 95P 149781
            PI MIHARA YASUHIRO, UDAGAWA TAKASHI, YAMADA HIDEAKI, PI ASANO
            YASUHIRO
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            CC topology: Linear;
            CC hypothetical: No;
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            FT mat_peptide
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            FT mutation
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LOCUS      AR384033
DEFINITION Sequence 762 from patent US 6610836.
ACCESSION AR384033
VERSION    AR384033.1
KEYWORDS   GI:40093767
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 762)
AUTHORS    Breton,G.L. and Osborne,M.
TITLE      Nucleic acid amino acid sequences relating to Klebsiella pneumoniae
            for diagnostics and therapeutics
JOURNAL    Patent: US 6610836-A 762 26-AUG-2003;
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 AB044338
 VERSION AB044338.1 GI:11610578
 KEYWORDS
 SOURCE Enterobacter aerogenes
 ORGANISM Enterobacter aerogenes
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Enterobacter.
 1 (sites)
 Miura, Y., Utagawa, T., Yatsui, H. and Asano, Y.
 Acid phosphatase/phosphotransferase from enteric bacteria
 Unpublished
 2 (bases 1 to 1650)
 Miura, Y. and Asano, Y.
 Direct Submission
 Submitted (06-JUN-2000) Yasuhiro Miura, Ajinomoto Co., Inc.,
 Fermentation & Biotechnology laboratories; Kawasaki-Ku,
 Kawasaki-shi, Kanagawa 210-8681, Japan
 (E-mail: yasuhiro.mihara@ajinomoto.com, Tel: 81-44-244-7138,
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 Location/Qualifiers
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ORIGIN

Query Match 41.8%; Score 512.2; DB 1; Length 1650;
 Best Local Similarity 79.3%; Pred. No. 1.9e-131; Indels 0; Gaps 0;
 Matches 607; Conservative 0; Mismatches 158;

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RESULT 11
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LOCUS
DEFINITION
Sequence 23 from patent US 6207435.
ACCESSION
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VERSION
AR140159.1 GI:14482655
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 747)
AUTHORS
Mihara, Y., Udagawa, T., Yamada, H. and Asano, Y.
TITLE
Method for producing nucleoside-5'-phosphate ester
JOURNAL
Patent: US 6207435-A 23 27-MAR-2001;
FEATURES
Location/Qualifiers
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Query Match 41.4%; Score 507; DB 6; Length 747;
Best Local Similarity 79.9%; Pred. No. 4.7e-130;
Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

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ACCESSION
E16587
VERSION
E16587.1 GI:5711270
KEYWORDS
JP 1998201481-A/4.
SOURCE
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ORGANISM
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REFERENCE
1 (bases 1 to 747)
AUTHORS
Mihara, Y., Udagawa, T., Yamada, H. and Asano, Y.
TITLE
PRODUCTION OF NUCLEOSIDE 5'-PHOSPHATE
JOURNAL
Patent: JP 1998201481-A 4 04-AUG-1998;
AJINOMOTO CO INC
COMMENT
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PN JP 1998201481-A/4
PD 04-AUG-1998
PF 18-JUN-1997 JP 1997161674
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Best Local Similarity 79.9%; Pred. No. 4.7e-130;
Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

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DEFINITION Sequence 23 from patent US 6355472.
ACCESSION AR199648
VERSION AR199648.1 GI:20249722
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 747)
AUTHORS Mihara,Y., Udagawa,T., Yamada,H. and Asano,Y.
TITLE Method for producing nucleoside-5'-phosphate ester
JOURNAL Patent: US 6355472-A 23 12-MAR-2002;
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Best Local Similarity 79.9%; Pred. No. 4.7e-130;
Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

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RESULT 14
LOCUS BD017677 747 bp DNA linear PAT 27-AUG-2002
DEFINITION Mutant acidic phosphatase.
ACCESSION BD017677
VERSION BD017677.1 GI:22558853
KEYWORDS JP 2001245676-A/12.
SOURCE Enterobacter aerogenes
ORGANISM Enterobacter aerogenes
REFERENCE 1 (bases 1 to 747)
AUTHORS Mihara,Y., Udagawa,T., Yamada,H. and Asano,Y.
TITLE Mutant acidic phosphatase
JOURNAL Patent: JP 2001245676-A 12 11-SEP-2001;
COMMENT AJINOMOTO CO INC
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    PN JP 2001245676-A/12
    PD 11-SEP-2001
    PF 26-DEC-2000 JP 2000395323
    PI YASUHIRO MIHARA,TAKASHI UDAGAWA,HIDEAKI YAMADA,YASUHIISA ASANO
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Search completed: June 4, 2004, 19:59:04
Job time : 3431 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 17:52:56 ; Search time 412 Seconds
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Title: US-09-807-990-1

Perfect score: 1225

Sequence: 1 ctgcagggaaggaagcaatgt.....taagatcatgtgcggttaac 1225

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 120%
Listing first 45 summaries

Database : N Geneseq_29Jan04.*

- 1: geneseqn1990s.*
- 2: geneseqn1990s.*
- 3: geneseqn2002s.*
- 4: geneseqn2003as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002s.*
- 7: geneseqn2003as.*
- 8: geneseqn2003bs.*
- 9: geneseqn2003cs.*
- 10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1225	100.0	1225	AAH19701	AAH19701 Escherich
2	750	61.2	750	AAH45011	AAH45011 Escherich
3	750	61.2	750	AAV43046	AAV43046 DNA encod
4	507	41.4	747	AAAT45007	AAAT45007 Enterobac
5	507	41.4	747	AAV43060	AAV43060 DNA encod
6	494.6	40.4	1650	AAH19705	AAH19705 Enterobac
7	435.4	40.3	747	AAH45008	AAH45008 Klebsiell
8	423.6	40.3	747	AAV43061	AAV43061 DNA encod
9	423.6	34.6	1344	AAH19702	AAH19702 Morganell
10	422	34.4	750	AAAT45010	AAAT45010 Morganell
11	422	34.4	750	AAV43045	AAV43045 DNA encod
12	357.4	29.2	747	AAAT45012	AAAT45012 Providenc
13	357.4	29.2	747	AAV43059	AAV43059 DNA encod
14	304.6	24.9	735	AAAT45009	AAAT45009 Serratia
15	304.6	24.9	735	AAV43062	AAV43062 DNA encod
16	162.2	13.2	1134	AAQ64128	AAQ64128 Virulence
17	160.6	13.1	1134	AAQ40878	AAQ40878 Apyrase {
18	141.6	11.6	991	AAH19703	AAH19703 Salmonell
19	91.8	7.5	1335	AAQ20191	AAQ20191 Zymomonas
20	85.4	7.0	756	AAQ20191	AAQ20191 Zymomonas
21	63	5.1	2300	ADA71938	ADA71938 Rice gene
22	58	4.7	5387	AAH19703	AAH19703 Salmonell
23	58	4.7	5387	AAH19703	AAH19703 Salmonell

24	51.6	4.2	2000	7	ADA71938	ADA71938 Rice gene
25	45.2	3.7	555	6	ABN24547	ABN24547 Human ORF
26	44.6	3.6	62909	4	AAF28545	AAF28545 Genomic f
27	44.6	3.6	349980	6	ABQ81842	ABQ81842 Bifidobac
28	39.6	3.2	1830	7	ACA37565	ACA37565 Prokaryot
29	37.8	3.1	5121	5	AAH81358	AAH81358 DNA encod
30	37.4	3.1	2310	6	ABH62750	ABH62750 Prostata
31	37.4	3.1	2310	7	ABX77539	ABX77539 Different
32	37.4	3.1	2310	8	ACH04005	ACH04005 Human CDN
33	37	3.0	930	7	ADA69509	ADA69509 Rice gene
34	37	3.0	1866	5	AAH66282	AAH66282 C glutami
35	37	3.0	1938	7	ACA00462	ACA00462 C. glutami
36	37	3.0	349980	5	AAH85828	AAH85828 C glutami
37	36.8	3.0	945	7	ABZ37548	ABZ37548 Streptomy
38	36.8	3.0	59816	7	ABZ37516	ABZ37516 Streptomy
39	36.8	3.0	59816	7	AAZ55887	AAZ55887 Sorangium
40	36.8	3.0	68750	3	AAZ55887	AAZ55887 Sorangium
41	36.8	3.0	71989	3	AAAT29349	AAAT29349 Sorangium
42	36.4	3.0	4696	2	AAAT13330	AAAT13330 Rat type
43	36.4	3.0	4696	9	ADB58713	ADB58713 Toxicity-
44	36.4	3.0	110000	4	AAI99682_16	Continuation (17 o
45	36.4	3.0	110000	4	AAI99683_16	Continuation (17 o

ALIGNMENTS

RESULT 1
AAH19701
ID AAH19701 standard; DNA; 1225 BP.
XX
AC AAH19701;
XX
DT 23-JUL-2001 (first entry)
XX
DE Escherichia blatae nucleotide-5'-phosphate producing enzyme DNA.
XX
BB Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;
transphosphorylation; phosphatase; protein co-ordinate data;
X-ray structural analysis; three-dimensional structure; ds.
XX
OS Escherichia blatae.
XX
PN WO200118184-A1.
XX
PD 15-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-JP005973.
XX
PR 03-SEP-1999; 95JP-00249545.
XX
PS (AJIN) AJINOMOTO CO INC.
XX
PI Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H;
Kurashiki O, Kouda T, Shimaoka M, Kozutsumi R, Asano Y;
XX
DR WPI; 2001-380914/40.
XX
PT P-PSDB; AAB75064.
XX
PT Variant enzyme having elevated nucleoside 5'-prime phosphate producing
activity and having a specific three-dimensional structure for production
of nucleotides as pharmaceutical intermediates.
XX
PS Disclosure; Page 105-106; 150pp; Japanese.
XX
CC The present invention describes a variant nucleoside-5'-phosphate
producing enzyme which is a modification of a transphosphorylase or
phosphatase which contains a lysine, two arginine and two histidine
residues and in which the C-alpha distances between these residues are
enclosing a space which permits the binding of a nucleoside with these
residues. Also described are: (1) a gene encoding the variant enzyme; (2)
expression vectors containing the DNA; (3) host cells transformed by the
vectors; (4) preparation of the variant enzyme by culture of the

CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
 CC with molybdenic acid; and (6) selection of inhibitors of acid phosphatase
 CC or transphosphorylase using the structural coordinates derived from the
 CC enzyme. The variant enzymes with increased efficiency for production of
 CC nucleoside 5'-phosphates can be used as pharmaceutical intermediates.
 CC AAH19701 to AAH19785 and AAH75064 to AAH75101 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 1225 B?; 280 A; 321 C; 339 G; 285 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1225; DB 4; Length 1225;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGCGAGCGAAGGCAATGTGGTGGCGGTGAGAGCGCACTCTACGAGATTAGGATAG 50
 DB 1 CTGCGAGCGAAGGCAATGTGGTGGCGGTGAGAGCGCACTCTACGAGATTAGGATAG 50
 QY 61 TAACATATCCATTATACAGTAAACAGCATTTGCTCTGAGTGTGATCTCATCTAGCGG 120
 DB 61 TAACATATCCATTATACAGTAAACAGCATTTGCTCTGAGTGTGATCTCATCTAGCGG 120
 QY 121 CGCGGGGGTTCGCCGGGCGCTTTTATGGGCTGCGGTGAGAGCGTTATCTGCTG 180
 DB 121 CGCGGGGGTTCGCCGGGCGCTTTTATGGGCTGCGGTGAGAGCGTTATCTGCTG 180
 QY 181 GCGCTGTGTGCAACAAAGCGTTTATTTGTTAAATTTTGTGACCTATATCAGGTTTT 240
 DB 181 GCGCTGTGTGCAACAAAGCGTTTATTTGTTAAATTTTGTGACCTATATCAGGTTTT 240
 QY 241 AAGCACCTGTGCGCTCTACTGCAACCTGTGTGATATTAAGCAACACTCTTCACTCAC 300
 DB 241 AAGCACCTGTGCGCTCTACTGCAACCTGTGTGATATTAAGCAACACTCTTCACTCAC 300
 QY 301 GGAATTAACACGCACAGTAAAGTATACGATGAAAGAAAGAGTGTCTTGGCAGTTGTTT 360
 DB 301 GGAATTAACACGCACAGTAAAGTATACGATGAAAGAAAGAGTGTCTTGGCAGTTGTTT 360
 QY 361 GCGCGATTGTTCTTCTCAGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 GCGCGATTGTTCTTCTCAGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 AAACCGGATCTCTACTACTCTCAAGACAGTGAAGCCATTAACAGCCCTGGCGCTGTTCGG 480
 DB 421 AAACCGGATCTCTACTACTCTCAAGACAGTGAAGCCATTAACAGCCCTGGCGCTGTTCGG 480
 QY 481 CCAACACCGGCGGTGGGCTCCATGCTTCTCAAGATCAGGCTATGATGACAGGGG 540
 DB 481 CCAACACCGGCGGTGGGCTCCATGCTTCTCAAGATCAGGCTATGATGACAGGGG 540
 QY 541 CGCTCTGCGCAACACCGAAGCGGTAACTGCGCGCGAAGATGCAAACTGAGCGGT 600
 DB 541 CGCTCTGCGCAACACCGAAGCGGTAACTGCGCGCGAAGATGCAAACTGAGCGGT 600
 QY 601 GCGCGGCTGCGGATGCTTTCTCGGCGGCTTTGGTAGCCCGATTCACGAAAAGAGCGCC 660
 DB 601 GCGCGGCTGCGGATGCTTTCTCGGCGGCTTTGGTAGCCCGATTCACGAAAAGAGCGCC 660
 QY 661 CCGGCGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
 DB 661 CCGGCGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
 QY 721 AGCGGAAAGATCACTATATGCGCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 DB 721 AGCGGAAAGATCACTATATGCGCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 781 AATACCAACCGAGGAGCAAACTCTCAAAAATGGCTCTTATCCGTCCGGGCACTACTCT 840
 DB 781 AATACCAACCGAGGAGCAAACTCTCAAAAATGGCTCTTATCCGTCCGGGCACTACTCT 840
 QY 841 ATCGGCTGGGCTACTGCGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB 841 ATCGGCTGGGCTACTGCGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

QY 901 CTGAAACCGGTTATGAGCTGGGCGCAGAGCCGGGTGATTGCGGCTACCACTGGCAGAGT 960
 DB 901 CTGAAACCGGTTATGAGCTGGGCGCAGAGCCGGGTGATTGCGGCTACCACTGGCAGAGT 960
 QY 961 GATGTGGATCGCGCGGGGTAGTGGATCTGCGTGTGCGGACCTGCTGATACCAACCG 1020
 DB 961 GATGTGGATCGCGCGGGGTAGTGGATCTGCGTGTGCGGACCTGCTGATACCAACCG 1020
 QY 1021 GCGTTCCAGCAGCAGTTGCGAGAAAGCGAAGCGCGAATTCGCCAGCATCAGAGAAATAA 1080
 DB 1021 GCGTTCCAGCAGCAGTTGCGAGAAAGCGAAGCGCGAATTCGCCAGCATCAGAGAAATAA 1080
 QY 1081 TCTGACTACCGCTTGCCTTGCAGGGCGGTAGTGTTCCTAGTCCCTGCGCGGATTCGCTAT 1140
 DB 1081 TCTGACTACCGCTTGCCTTGCAGGGCGGTAGTGTTCCTAGTCCCTGCGCGGATTCGCTAT 1140
 QY 1141 TCCACAGTAAATGACGCGTATATGATTGTCGCAACGAAAGGTTGTGTACGCGCACA 1200
 DB 1141 TCCACAGTAAATGACGCGTATATGATTGTCGCAACGAAAGGTTGTGTACGCGCACA 1200
 QY 1201 GCTTATAAGCATCATGTCGCGTTAAAC 1225
 DB 1201 GCTTATAAGCATCATGTCGCGTTAAAC 1225
 RESULT 2
 AAT45011
 ID AAT45011 standard; DNA; 750 BP.
 XX AAT45011;
 AC AC
 XX DT
 XX 13-AUG-1997 (first entry)
 DE Escherichia blattae JCM 1650 acid phosphatase DNA.
 XX JCM 1650; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
 KW condiment; pharmaceutical; intermediate; ds.
 XX Escherichia blattae.
 Key Location/Qualifiers
 CDS 1..750
 /tag= a
 /product= "acid_phosphatase"
 sig_peptide 1..54
 /tag= b
 mat_peptide 55..747
 /tag= c
 WO9637603-A1.
 PN 28-NOV-1996.
 PO 24-MAY-1996; 96WO-JP001402.
 XX 25-MAY-1995; 95JP-00149781.
 PR 26-MAR-1996; 96JP-00094680.
 XX (AJIN) AJINOMOTO CO INC.
 PA Mihara Y, Utagawa T, Yamada H, Asano Y;
 PI WPI; 1997-021215/02.
 DR P-2SDB; AAW06463.
 XX Efficient production of nucleoside 5'-phosphate - by reactor of a
 PT nucleoside with a phosphoric acid donor in the presence of an acid
 PT phosphatase.
 XX Example 16; Page 56-58; 95pp; Japanese.
 PS The present sequence encodes the Escherichia blattae JCM 1650 acid
 CC

CC phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
CC -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
CC 3.0 to 5.5. The PA can be used for the economic and efficient production
CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
CC and intermediates for pharmaceuticals
XX
SQ Sequence 750 BP; 170 A; 212 C; 217 G; 151 T; 0 U; 0 Other;

Query Match 61.2%; Score 750; DB 2; Length 750;
Best Local Similarity 100.0%; Pred. No. 3.4e-225;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 ATGAAAAAGCTGCTTGGCAGTTTGTGTTTGGCGCATTTCTTCTCAGGCGCTGGCG 390
DB 1 ATGAAAAAGCTGTTCTGGCAGTTTGTGTTTGGCGCATTTCTTCTCAGGCGCTGGCG 60

QY 391 CTGGTCGCTACCGGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACGT 450
DB 61 CTGGTCGCTACCGGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACGT 120

QY 451 GAAGCCATTAAACAGCTGGCGCTGTTGCGCGCACACGCGGGTGGGCTCCATTGCGTTT 510
DB 121 GAAGCCATTAAACAGCTGGCGCTGTTGCGCGCACACGCGGGTGGGCTCCATTGCGTTT 180

QY 511 CTCAACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGGCGCAACCGAACGCGGTAAG 570
DB 181 CTCAACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGGCGCAACCGAACGCGGTAAG 240

QY 571 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTTCTCCGCGCGG 630
DB 241 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTTCTCCGCGCGG 300

QY 631 TTGCGTACCGGATCACCAGAAAGAGCCCGGGTGGCAATTAATCTACCAATATG 690
DB 301 TTGCGTACCGGATCACCAGAAAGAGCCCGGGTGGCAATTAATCTACCAATATG 360

QY 691 ATTGAGGAGCGCGGGATCTGGCGACCGCGAGCGGCAAGATCACTATATCGCATTCGT 750
DB 361 ATTGAGGAGCGCGGGATCTGGCGACCGCGAGCGGCAAGATCACTATATCGCATTCGT 420

QY 751 CCGTTGCGTTTATGCGGCTCTTACCTGTATACCGAGCGAGGACAACTGTCCAAA 810
DB 421 CCGTTGCGTTTATGCGGCTCTTACCTGTATACCGAGCGGACAACTGTCCAAA 480

QY 811 AATGGCTCTTATCGTCCGGGCACTACCTCTATCGGCTGGCTACTGCGCTGTCTGGCA 870
DB 481 AATGGCTCTTATCGTCCGGGCACTACCTCTATCGGCTGGCTACTGCGCTGTCTGGCA 540

QY 871 GAGATCAACCTCAGCGCGCAGAACGAGATCTGAAACCGGTTATGACTGGGCGAGGC 930
DB 541 GAGATCAACCTCAGCGCGCAGAACGAGATCTGAAACCGGTTATGACTGGGCGAGGC 600

QY 931 CGGCGATTTCGGGCTACCACTGGCAGAGTGAATGAGTGGCGCGGCTAGTGGATCT 990
DB 601 CGGCGATTTCGGGCTACCACTGGCAGAGTGAATGAGTGGCGCGGCTAGTGGATCT 660

QY 991 GCGGTTGTGGGACCCCTGCATACCAACCGCGGTTCCAGAGCAGTTCGAGAAACGGAAG 1050
DB 661 GCGGTTGTGGGACCCCTGCATACCAACCGCGGTTCCAGAGCAGTTCGAGAAACGGAAG 720

QY 1051 GCCGAATTGCGCCAGCATCAGAAAGATAA 1080
DB 721 GCCGAATTGCGCCAGCATCAGAAAGATAA 750

RESULT 3
AAV43046
ID AAV43046 standard; DNA; 750 BP.
XX AAV43046;
XX
XX
DT 21-OCT-1998 (first entry)

XX DNA encoding an acid phosphatase enzyme.
DE Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW intermediate; ds.
XX
XX Escherichia blattae.
OS
XX Key Location/Qualifiers
FH CDS 1..750
FT /*tag= a
FT sig_peptide 1..54
FT /*tag= b
FT mat_peptide 55..747
FT /*tag= c
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
XX
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX
XX WPI: 1998-416010/36.
XX
XX P-PSDB; AAW71029.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX Example 12; Page 34-35; 83pp; English.
XX
XX The present sequence encodes an acid phosphatase enzyme. The
XX specification describes a method for the preparation of nucleoside 5'-
XX phosphate esters. The method comprises reacting a nucleoside with a
XX phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
XX has been altered to increase its affinity for the nucleoside and/or to
XX increase its thermal stability, or in the presence of a microorganism
XX that has been transformed with recombinant DNA containing a gene coding
XX for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
XX seasonings or pharmaceuticals or as intermediates for them
XX
SQ Sequence 750 BP; 170 A; 212 C; 217 G; 151 T; 0 U; 0 Other;

Query Match 61.2%; Score 750; DB 2; Length 750;
Best Local Similarity 100.0%; Pred. No. 3.4e-225;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 ATGAAAAAGCTGTTCTGGCAGTTTGTGTTTGGCGCATTTCTTCTCAGGCGCTGGCG 390
DB 1 ATGAAAAAGCTGTTCTGGCAGTTTGTGTTTGGCGCATTTCTTCTCAGGCGCTGGCG 60

QY 391 CTGGTCGCTACCGGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACGT 450
DB 61 CTGGTCGCTACCGGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACGT 120

QY 451 GAAGCCATTAAACAGCTGGCGCTGTTGCGCGCACACGCGGGTGGGCTCCATTGCGTTT 510
DB 121 GAAGCCATTAAACAGCTGGCGCTGTTGCGCGCACACGCGGGTGGGCTCCATTGCGTTT 180

QY 511 CTCAACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGGCGCAACCGAACGCGGTAAG 570
DB 181 CTCAACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGGCGCAACCGAACGCGGTAAG 240

QY 571 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTTCTCCGCGCGG 630
DB 241 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTTCTCCGCGCGG 300

QY 631 TTTGTAGCCGATCACCGAAGAGCCCGCGCTGCATATTAATCTAGCAATATG 690
 DB 301 TTTGTAGCCGATCACCGAAGAGCCCGCGCTGCATATTAATCTAGCAATATG 360
 QY 691 ATTGAGGAGCGCGGGATCTGGCGACCCGCGAGCGGAAAGATCACTATATGCGCATTCGT 750
 DB 361 ATTGAGGAGCGCGGGATCTGGCGACCCGCGAGCGGAAAGATCACTATATGCGCATTCGT 420
 QY 751 CCGTTCGGCTTTTATGCGGTCTCTACCTGTAATACACCGAGCGACAACCTCTCCAAA 810
 DB 421 CCGTTCGGCTTTTATGCGGTCTCTACCTGTAATACACCGAGCGACAACCTCTCCAAA 480
 QY 811 ATGCTCTTATCCGTCGGGCATACCTCTATCGGCTGGCTACTCGCTGGTGGTGCGCA 870
 DB 481 ATGCTCTTATCCGTCGGGCATACCTCTATCGGCTGGCTACTCGCTGGTGGTGCGCA 540
 QY 871 GAGATCAACCTCAGCGCCAGAACGAGATCCTGAAACGCGGTATGAGCTGGGCCAGAGC 930
 DB 541 GAGATCAACCTCAGCGCCAGAACGAGATCCTGAAACGCGGTATGAGCTGGGCCAGAGC 600
 QY 931 CCGGTGATTTGGCTTACACCTGCGAGAGTGATGTGATGCGCGCGGCTAGTGGATCT 990
 DB 601 CCGGTGATTTGGCTTACACCTGCGAGAGTGATGTGATGCGCGCGGCTAGTGGATCT 660
 QY 991 GCGGTGCGGACCTCGCATACCAACCGCGCTTCCAGCAGCAGTTGCAGAAAGCGAAG 1050
 DB 661 GCGGTGCGGACCTCGCATACCAACCGCGCTTCCAGCAGCAGTTGCAGAAAGCGAAG 720
 QY 1051 GCGGAATTCGCCAGCATCAGAAATAA 1080
 DB 721 GCGGAATTCGCCAGCATCAGAAATAA 750

RESULT 4

AAAT45007

ID AAT45007 standard; DNA; 747 BP.

XX AC AAT45007;

XX DT 13-AUG-1997 (first entry)

XX DE Enterobacter aerogenes IFC 12010 acid phosphatase DNA.

XX KW IFC 12010; acid phosphatase; production; nucleoside; 5'-phosphate; ester;

XX OS condiment; pharmaceutical; intermediate; ds.

XX OS Enterobacter aerogenes.

XX FH Key Location/Qualifiers

XX FT CDS 1..747

XX FT FT /*tag= a

XX FT FT /product= "acid_phosphatase"

XX PN WO9637603-A1.

XX PD 28-NOV-1996.

XX PF 24-MAY-1996; 96WO-JP001402.

XX PR 25-MAY-1995; 95JP-00149781.

XX PR 26-MAR-1996; 96JP-00094680.

XX PR (AJIN) AJINOMOTO CO INC.

XX PI Minara Y, Utagawa T, Yamada H, Asano Y;

XX DR WPI; 1997-021215/02.

XX DR P-PSDB; AAW06458.

XX PT Efficient production of nucleoside 5'-phosphate - by reaction of a

XX PT nucleoside with a phosphoric acid donor in the presence of an acid

XX PT phosphatase.

XX

PS Example 24; Page 67-68; 95pp; Japanese.

XX The present sequence encodes the Enterobacter aerogenes IFC 12010 acid
 CC phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
 CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
 CC -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
 CC 3.0 to 5.5. The PA can be used for the economic and efficient production
 CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
 CC and intermediates for pharmaceuticals

XX SQ Sequence 747 BP; 181 A; 210 C; 205 G; 151 T; 0 U; 0 Other;

Query Match 41.4%; Score 507; DB 2; Length 747;

Best Local Similarity 79.9%; Pred. No. 1.2e-148;

Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 331 ATGAAAACGTTCTGCGCAGTTGTTTGGCGCATTTGTTCTCTCTAGGCCCTGGCG 390

DB 1 ATGAAAACGTTCTGCGCAGTTGTTTGGCGCATTTGTTCTCTCTAGGCCCTGGCG 60

QY 391 CTGGTCGTACCGGCAACGACACTACCGAGAAACCGGATCTCTACTACCTCAGAACAGT 450

DB 61 CTGGTCGTACCGGCAACGACACTACCGAGAAACCGGATCTCTACTACCTCAGAACAGT 420

QY 451 GAAGCATTAACAGCTGCGGCTGTTGCGGCCACACCGCGGCTGCGCTCCATGCGTTT 510

DB 121 CAGGCCATCGATAGTCTGCGGCTGTTGCGGCCACACCGCGGCTGCGCTCCATGCGTTT 180

QY 511 CTCAAGCATCAGGCCATGATGAAACGAGGCGCTGCTGGCGCAACCGAACCGGTAAG 570

DB 181 TTAACGATCAGGCCATGATGAAACGAGGCGCTGCTGGCGCAACCGAACCGGTAAG 240

QY 571 CTGGCGCGGAGAGATGCAACCTGAGCAGTGGCGGCTGGCGAATGTTCTCCGGCGCG 630

DB 241 CTGGCGCGTGAAGATGCTAAGCTGAGCGCGCGGCGCTGCGAATGCTTCCAGCGCT 300

QY 631 TTTGGTAGCCGATCACCAGAAAGAGCGCCCGCGCTGCGAATGTTCTTCTGCGCGCG 690

DB 301 TTTGGTAGCCGATCACCAGAAAGAGCGCCCGCGCTGCGAATGCTTCTTCTGCGCGCG 360

QY 691 ATTGAGAACCGCGGATCTGGCGACCCGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 750

DB 361 ATTGAGAACCGCGGATCTGGCGACCCGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 420

QY 751 CCGTTCCGCTTTATGCGGCTCTCTACTGTAATACCGAGCAGGACAACTGTCGCGG 810

DB 421 CCGTTCCGCTTTATGCGGCTCTCTACTGTAATACCGAGCAGGACAACTGTCGCGG 480

QY 811 AATGGCTTTATCCGTCGGGCATACCTCTATCGGCTGGGCTACTGCGCTGCTGGCGCA 870

DB 481 AATGGCTTTATCCGTCGGGCATACCTCTATCGGCTGGGCTACTGCGCTGCTGGCGCA 540

QY 871 GAGATCAACCTCAGCGCCAGAACGAGATCCTGAAACCGCGGTTATGAGCTGGCGCG 930

DB 541 GAGATCAACCTCAGCGCCAGAACGAGATCCTGAAACCGCGGTTATGAGCTGGCGCG 600

QY 931 CCGGTGATTTGCGGCTACCACTGCGCAGAGTATGTTGATGCGCGCGGCTAGTGGATCT 990

DB 601 CCGGTGATTTGCGGCTACCACTGCGCAGAGTATGTTGATGCGCGCGGCTAGTGGATCT 660

QY 991 GCCGTTGCGGACCTGCGCATACCAACCGCGGTTCCAGCAGCAGGTTGCGAGAACGGAAG 1050

DB 661 GCCGTTGCGGACCTGCGCATACCAACCGCGGTTCCAGCAGCAGGTTGCGAGAACGGAAG 720

QY 1051 GCCGATTTGCCCGCAGCATCAGAAATAA 1077

DB 721 GATGAATTCGCCAAACCGCAGAGTAA 747

RESULT 5

AAV43060

ID AAV43060 standard; DNA; 747 BP.

XX AAV43060;
 AC 21-OCT-1998 (first entry)
 XX
 DT
 XX
 XX DNA encoding an acid phosphatase enzyme.
 DE
 XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 XX intermediates; GS.
 KW
 XX Enterobacter aerogenes.
 OS
 XX
 XX
 XX Key Location/Qualifiers
 PE 1. 747
 FT CDS /*tag= a
 FT
 XX
 XX EF857788-A2.
 PN
 XX
 XX 12-AUG-1998.
 PD
 XX
 XX 20-NOV-1997; 97EP-00309365.
 PF
 XX
 XX 21-NOV-1996; 96JP-00311103.
 PR
 XX 18-JUN-1997; 97JP-00161674.
 XX
 XX (AJIN) AJINOMOTO CO INC.
 PA
 XX
 XX Mihara Y, Utagawa T, Yamada H, Asano Y;
 PI
 XX
 XX WPI; 1998-416010/36.
 XX P-PSDB; AAW71031.
 DR
 XX
 XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.
 PT
 XX
 XX Example 24; Page 43; 83pp; English.
 PS
 XX
 XX The present sequence encodes an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC that has been transformed with recombinant DNA containing a gene coding
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them
 XX
 XX Sequence 747 BP; 181 A; 210 C; 205 G; 151 T; 0 U; 0 Other;
 SQ
 Query Match 41.4%; Score 507; DB 2; Length 747;
 Best Local Similarity 79.9%; Pred. No. 1.2e-148;
 Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
 QY 331 ATGAAAAACGTTCTGCGAGTTGTTTTCGCGATTGTTCTCTCTCAGGCCCTCGCG 390
 DB 1 ATGAAAAAGCGGTTCTGCGCTCTGCGCTGCGAGCTGTTTCGTTAAAGCTTTGCG 60
 QY 391 CTGTCGTCTACGGGACGACACTACACGAAACCGGATCTCTACTACTCAAGAACAGT 450
 DB 61 CTGTCCTCTGCGGCAATGATGCAACCAACCGGATCTCTATTATCTGAAAAATGCA 120
 QY 451 GAAGCCATTAACAGCTGCGCTGTTGCGCCACCCAGCGGCTGCGCTCAATTGCGTTT 510
 DB 121 CAGCCATTCGATGTTCTGCGCTGTTGCGCGCCGCGGAGTTGGAGCATTCGCAATT 180
 QY 511 CTCACGATCAGGCCATGATGAAACAGGGCGCGCTGTCGCGCAACCGAAGCGGTAAG 570
 DB 181 TTAACGATCAGCGGATGATGAGAAAGGACGCGCTGTTGCGCAATACCGAAGCTGCGAAG 240
 QY 571 CTGCGCGCGGAGATGCAAACTGAGCAGTGGCGGGGTGGGCAATGCTTCTCCGCGCG 530
 DB 241 CTGCGCGCTGAAGATGCTAAACCTGAGCGCGCGCGCTGCGCAATGCTTCTCCAGCGCT 300

QY 631 TTTGGTAGCCCGATCACCGAAAAAGAGCCCGCGCTGCATAAATTACTGACCAATATG 690
 DB TTTGGTTGCGCCATCACCGAAAAAGAGCGCGCGAGTTACATAAGCTGCTGCAATATG 360
 QY 691 ATTGAGGACGCGGGGATCTGGGACCGCGAGCGGAAAGATCATATATCGCATTCGT 750
 DB ATTGAGGATGCGGCGATCTGGCCACCGCGAGCGGAAAGAAATATATCGCATTCGC 420
 QY 751 CCGTTCCGGTTTATGGGTTCTTACCTGTAAATACCCGAGGAGGACAAACTGTCCAAA 810
 DB CCGTTTCGGTTCTACGGCGTTTCAACCTGTAACTACCGAGGAGGACAGCTGTGAAA 480
 QY 811 AATGCTCTTTATCCGTCGGGCATACCTCTATCGGCTGGGCTACTGCGCTGGTGTGCA 870
 DB AACGATCTTACCTTTCGGCCATACCTCTATCGTTGGGCAACCGCGCTGGTACTGCG 540
 QY 871 GAGATCAACCTCTAGCGCGAGAACGAGATCTGAAAACGCGTTATGACTGGCCAGAGC 930
 DB GAGATCAATCGCAGCGGCAAAACGAAATTTCTAAACGCGCTATGAATTGGGCGAAAGC 600
 QY 931 CGGTTGATTTTCGGCTACCTGCGCAGATGATGTGGATGCGCGCGGCTAGTGGGATCT 990
 DB CGGTTATCTCGGCTATCATTTGGCAGAGCGATGTGATGCGGCGCGGATCTCGGCTCG 660
 QY 991 GCCGTTGTGCGACCTCTGCATACCAACCGCGCTTCCAGCAGCATTCGAGAAACGGAAG 1050
 DB GCGTGTGCGGACCTCTGCATACCAACCGCGCTTCCAGCAGCATTCGAGAAACGGAAG 720
 QY 1051 GCCGAATTCGCGCCAGCATCGAAGAA 1077
 DB GATGAATTCGCCAAACGCGAAGTAA 747

RESULT 6

AAH19705
 ID AAH19705 standard; DNA; 1450 BP.

XX AC AAH19705;

XX DT 23-JUL-2001 (first entry)

XX DE Enterobacter aerogenes nucleotide-5'-phosphate producing enzyme DNA.

XX KW Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;

XX KW transphosphorylation; phosphatase; protein co-ordinate data;

XX KW X-ray structural analysis; three-dimensional structure; ds.

XX OS Enterobacter aerogenes.

XX FN WO200118184-A1.

XX PD 15-MAR-2001.

XX PF 01-SEP-2000; 2000WO-JP005973.

XX PR 03-SEP-1999; 99JP-00249545.

XX (AJIN) AJINOMOTO CO INC.

XX PI Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H;

XX PI Kurahashi O, Kouda T, Shimaoka M, Kozutsumi R, Asano Y;

XX DR WPI; 2001-380914/40.

XX P-PSDB; AAB75068.

XX PT Variant enzyme having elevated nucleoside 5'-prime phosphate producing
 activity and having a specific three-dimensional structure for production
 of nucleotides as pharmaceutical intermediates.

XX PS Disclosure; Page 115-117; 150pp; Japanese.

XX CC The present invention describes a variant nucleoside-5'-phosphate

CC producing enzyme which is a modification of a transphosphorylase or
CC phosphatase which contains a lysine, two arginine and two histidine
CC residues and in which the C-alpha distances between these residues are
CC enclosing a space which permits the binding of a nucleoside with these
CC residues. Also described are: (1) a gene encoding the variant enzyme; (2)
CC expression vectors containing the DNA; (3) host cells transformed by the
CC vectors; (4) preparation of the variant enzyme by culture of the
CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
CC with molybdenic acid; and (6) selection of inhibitors derived from the
CC or transphosphorylase using the structural coordinates of acid phosphatase
CC enzyme. The variant enzymes with increased efficiency for production of
CC nucleoside 5'-phosphates can be used as pharmaceutical intermediates.
CC AAH13701 to AAH1785 and AAB75064 to AAB75101 represent sequences used in
CC the exemplification of the present invention

XX SQ Sequence 1650 BP; 401 A; 461 C; 433 G; 355 T; 0 U; 0 Other;

Query Match 40.4%; Score 494.6; DB 4; Length 1650;
Best Local Similarity 77.9%; Pred. No. 1.4e-144;
Matches 596; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 313 CACAGTAAGGTATACGCATGAAACAAAGTGTCTCTGCGAGTTTCTTTGCGCATTTGTC 372
DB |||||
QY 326 CACGTAAGGAATGTAGATGAAACAGCGTCTCTGCGCTCTGCGCATTTGTC 385
DB |||||
QY 373 TCTTCTCAGGCGCTGCTGCTACCGGCAACGACATACACGAAACCGGATCTC 432
DB |||||
QY 386 TCGGTAACGCTTCGCGCTGCTCCCTGCGGCAATGATCAACACCAACCGGATCTC 445
DB |||||
QY 433 TACTACTCAAGAACAGTGAAGCAATTAACAGCCTGCGGCTGTGCGGCAACCGGCG 492
DB |||||
QY 446 TATTATCTGAATAATGCACAGGCGCATGATGCTGCGGCTGTGCGGCGCGCGGAA 505
DB |||||
QY 493 GTGGGTCCTATGCTTCTCAAGATCAGCCCATGTATGAACAGGCGCGCTGTCGCG 552
DB |||||
QY 506 GTTGGCAGATCGCTTTTAAAGATCAGCGATGTATGAAAGAGCGCTGTGCGG 565
DB |||||
QY 553 AACACCGAAACCGGTAAAGTGGCGCGGAAGATCAACACCTGAGTGTGGCGGCTGCGG 612
DB |||||
QY 566 AATACCGAAGTGCACAGGCGCGGAGATGCTGACCTGCGCGCGGCGAGCTGCGG 625
DB |||||
QY 613 AATGCTTCTCGCGCGCTTGTGTAGCCCGATCAACGAAAGAGCGCGCGCGCTGAT 672
DB |||||
QY 626 AATGCTTCTCGCGCGCTTGTGTAGCCCGATCAACGAAAGAGCGCGCGCGCTGAT 685
DB |||||
QY 673 AATTAAGTACCAATGATGAGAGCGCGGATCTGGCGACCGCGAGCGCAAGAT 732
DB |||||
QY 686 AAGCTGCTGACAAATGATGAGATGCGCGGATCTGGCCACCGCGAGCGCAAGAG 745
DB |||||
QY 733 CACTATATGCGCATTCGTCGCTGCGGTTTATGCGGCTCTACTGTAATACCGAG 792
DB |||||
QY 746 AATATATGCGCATTCGCGCTTGTGTAGCGGCTTCAACCTGTAACTAAAGAC 805
DB |||||
QY 793 CAGGACAACTCTCAAAATGCTCTTATCGGTCGCGGATCTCTATCGCTGCGGT 852
DB |||||
QY 806 CAGGACAACTCTCAAAATGCTCTTATCGGTCGCGGATCTCTATCGCTGCGGT 865
DB |||||
QY 853 ACTGCGTGTGCTGCGAGATCAACCTCAGCGCCAGAGAGATCTCTCAAAACGCGGT 912
DB |||||
QY 866 ACCGCGTGTGCTGCGGATCAATCGCGAGCGGCAAGCAATCTCAACCGCGG 925
DB |||||
QY 913 TATGAGCTGGGCGAGACCGGCTGATTTGCGGCTACCACTGGCAGAGTGTGATGCC 972
DB |||||
QY 926 TATGAATTGGCGAAACCGGCTTATCTGCGCTATCATTTGGCAGAGGATGTGATGCG 985
DB |||||
QY 973 GCGGGGTAGTGGATCTGCGGTTGTGGCGACCTTGATCAACACCGGCTTCCAGCG 1032
DB |||||
QY 986 GCGGGGTAGTGGATCTGCGGTTGTGGCGACCTTGATCAACACCGGCTTCCAGCG 1045
DB |||||
QY 1033 CAGTTGCGAAGCGAAGCGAATTTGCGCGAGCATCAGAGAA 1077
DB |||||
QY 1046 CAGTTGCGAAGCGAAGCGAATTTGCGCGAGCATCAGAGAA 1090
DB |||||

RESULT 7

AAAT45008
ID AAAT45008 standard; DNA; 747 BP.

XX AC AAAT45008;

XX DT 17-OCT-2003 (revised)
XX DT 13-AUG-1997 (first entry)

XX Klebsiella planticola IFO 14939 acid phosphatase DNA.

XX IFO 14939; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
XX condiment; pharmaceutical; intermediate; ds.

XX Raoultella planticola.

XX Key Location/Qualifiers

XX CDS 1..747

XX /*tag= a
XX /product= "acid_phosphatase"

XX MO3637603-A1.

XX 28-NOV-1996.

XX 24-MAY-1996; 96WO-JP001402.

XX 25-MAY-1995; 95JP-00149781.

XX 26-MAR-1996; 96JP-00094680.

XX (AJIN) AJINOMOTO CO INC.

XX Mihara Y, Utagawa T, Yamada H, Asano Y;

XX WPI; 1997-021215/02.

XX P-FSD; AHW08459.

XX Efficient production of nucleoside 5'-phosphate - by reaction of a
XX nucleoside with a phosphoric acid donor in the presence of an acid
XX phosphatase.

XX Example 24; Page 70-72; 95pp; Japanese.

XX The present sequence encodes the Klebsiella planticola IFO 14939 acid
XX phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
XX ester from the corresponding nucleoside when a phosphate donor, e.g. poly
XX -phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
XX 3.0 to 5.5. The PA can be used for the economic and efficient production
XX of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
XX and intermediates for pharmaceuticals. (Updated on 17-OCT-2003 to
XX standardise OS field)

XX Sequence 747 BP; 168 A; 230 C; 209 G; 140 T; 0 U; 0 Other;

Query Match 40.3%; Score 493.4; DB 2; Length 747;

Best Local Similarity 79.0%; Pred. No. 2.2e-144;

Matches 587; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 331 ATGAAAAACGTTCTGCGAGTTTGTTCGCGCATTTGTTCTCTCTCAGGCCCTTGGG 390

DB |||||

DB 1 ATGAAAAAGGTGTACTCGCCCTTGTGCGAGCCCTTTTCAGTTAGCGCTTGGG 60

QY 391 CTGTCGCTACCGCAACGACATACCAAGAAACGGATCTCTACTCTCAAGAACAGT 450

DB |||||

DB 61 CTGTTCCCGCGCAATGATGCCACCAAGCCGATCTCTACTATCTGAAAAATGCC 120

QY 451 GAAGCATTAACAGCTGGCGCTGTTCGCGCAACACCGCGGTGGCTCCATTCCGTT 510

DB |||||

DB 121 CAGGCCATTGACGCTGGCGCTGTTCGCGCGCGGAAAGTGGGAGCATTCGCTT 180

QY 511 CTCACGATCAGGCGCATGTATGAACAGGCGGCGCTGTTCGCGCAACACCGCGGTAG 570

DB |||||

Db 181 TTAACGATCAGCGATGATGAGAAGCGCTCTCTCGCGCCACCGCCCGCGCAAG 240
QY 571 CTGGCGCGGAGATCAAACTTGAGCAGTGGCGGGTGGCGAATGCTTTCTCGCGCG 630
Db 241 TTGGCGCGGAGATGCAACCTGAGCGGGTGGCGTGGCGCAACGCTTTCTCGCGAGCA 300
QY 631 TTTGGTAGCCGATCACCAGAAAGAGCGCCCGCGCTGCATTAATTAAGTACCAATATG 690
Db 301 TCGCGCTCCCGATCAGCAAAAGAGCGCCCGCGCTGCATTAATTAAGTACCAATATG 360
QY 691 ATTGAGACGCGGGGATCTGGCAGCCCGCAGCGGAAAGATCACTATATGCGGATCGT 750
Db 361 ATTGAGACGCGGGGATCTGGCAGCCCGCAGCGGAAAGATCACTATATGCGGATCGT 420
QY 751 CCGTTCGCTTTTANGGGTCTTACCTGTAAATACCAACCGAGGAGCAAACTGTCAAA 810
Db 421 CCGTTTGCCTTTACGGCGTGTCCACCTGCAATACCAACCGAGGATTAAGCTGCAAA 480
QY 811 AATGGCTCTTATCGTGGGATACCTCTATCGCTGGGCTACTGCGCTGGTGTGGCA 870
Db 481 AAGCGCTCTTACCGCTTCCGACACACCTCTATCGCTGGGCTGGGCTGGTGGCC 540
QY 871 GAGATCAACCTCAGCGCCAGACGAGATCTCTGAAACCGGTTATGACTGGGCCAGAGC 930
Db 541 GAAATCAACCGCAGCGCCAGATGAGATTCTCAAGCGCGGCTATGAGCTCGGTCAAA 600
QY 931 CCGGTGATTTGGCGTACCACTGCGAGAGTATGAGTGGATGGCGCGGGTAGTGGATCT 990
Db 601 CCGGTGATTTGGCGTACCACTGCGAGAGTATGAGTGGATGGCGCGGGTAGTGGATCT 660
QY 991 GCGGTGATTTGGCGTACCACTGCGAGAGTATGAGTGGATGGCGCGGGTAGTGGATCT 1050
Db 661 GCGGTGATTTGGCGTACCACTGCGAGAGTATGAGTGGATGGCGCGGGTAGTGGATCT 720
QY 1051 GCCGAATTCGCCAGCATCAGAA 1073
Db 721 GACGAGTTTGGAAACAGCAGAA 743

RESULT 8
AAV43061
ID AAV43061 standard; DNA; 747 BP.
AC AAV43061;
XX
XX 27-AUG-2003 (revised)
DT 21-OCT-1998 (first entry)
DE
DE DNA encoding an acid phosphatase enzyme.
XX
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW intermediate; ds.
XX
XX Raoultella planticola.
XX
FH Key Location/Qualifiers
FT CDS 1..747
FT /*tag= a
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
PD
XX 20-NOV-1997; 97EP-00309365.
PF
XX 21-NOV-1996; 96JP-00311103.
PR
XX 18-JUN-1997; 97JP-00161674.
PR
XX (AJIN) AJINOMOTO CO INC.
PA
XX Miura Y, Utagawa T, Yamada H, Asano Y;
PI WPI; 1998-416010/36.
XX
DR

P-PSDB; AAW71032.
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
XX
XX Example 24; Page 45-46; 83pp; English.
PS
XX The present sequence encodes an acid phosphatase enzyme. The
CC specification describes a method for the preparation of nucleoside 5'-
CC phosphate esters. The method comprises reacting a nucleoside with a
CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
CC has been altered to increase its affinity for the nucleoside and/or to
CC increase its thermal stability, or in the presence of a microorganism
CC that has been transformed with recombinant DNA containing a gene coding
CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
CC seasonings or pharmaceuticals or as intermediates for them. note: this
CC sequence appears to be claimed (Claim 6), but as the claim refers to
CC amino acid sequences, it is clear that the corresponding protein is
CC being claimed. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 747 BP; 168 A; 230 C; 209 G; 140 T; 0 U; 0 Other;
Query Match 40.3%; Score 493.4; DB 2; Length 747;
Best Local Similarity 79.0%; Pred. No. 2.2e-144;
Matches 587; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 331 ATGAAAAAAGCTGTCTCGCAGTTTGTGTCGCAATGTTCTCTTCTCAGGCCCTTGGCG 390
Db 1 ATGAAAAAAGCTGTCTCGCAGTTTGTGTCGCAATGTTCTCTTCTCAGGCCCTTGGCG 60
QY 391 CTGTGCTCTACCGCAACGACACTACCAACGAAACCGGATCTCTACTCTCAAGACAGT 450
Db 61 CTGTGCTCTACCGCAACGACACTACCAACGAAACCGGATCTCTACTCTCAAGACAGT 120
QY 451 GAAGCCATTACAGCTGGCGCTGTGGCGCCACACCGCGGGTGGCTCCATTGGCTTT 510
Db 121 CAGGCCATTGACAGCTGGCGCTGTGGCGCCACCGCGGGTGGCTCCATTGGCTTT 180
QY 511 CTCACGATCAGCGCATGTATGAACAGGGCGCGCTCTGTCGCAACACCGGATGAG 570
Db 181 TTAACGATCAGCGCATGTATGAAGAGCCCTCTGTCGCGCCACCGCCCGCGCAAG 240
QY 571 CTGGCGCGGAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTTCTCGCGCG 630
Db 241 TTGGCGCGGAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTTCTCGCGAGCA 300
QY 631 TTTGGTAGCCGATCACCAGAAAGAGCGCCCGCGCTGCATTAATTAAGTACCAATATG 690
Db 301 TTTGGCTCTCCGATCAGCGGAAAGAGCGCCCGCGCTGCATTAATTAAGTACCAATATG 360
QY 691 ATTGAGGACGCGGGATCTGCGACCCCGCAGCGCGGAAAGATCACTATATGCGCATTCGT 750
Db 361 ATTGAGGACGCGGGATCTGCGACCCCGCAGCGCGGAAAGATCACTATATGCGCATTCGT 420
QY 751 CCGTTTGGCTTTTATGGGCTCTCTACTCTGCGCTGGGCTACTGCGTGGTCTGGCA 810
Db 421 CCGTTTGGCTTTTATGGGCTCTCTACTCTGCGCTGGGCTACTGCGTGGTCTGGCA 480
QY 811 AATGGCTCTTATCGTGGGCTATACCTCTATCGCTGGGCTACTGCGTGGTCTGGCA 870
Db 481 AATGGCTCTTATCGTGGGCTATACCTCTATCGCTGGGCTACTGCGTGGTCTGGCA 540
QY 871 GAGATCAACCTCAGCGCCAGACGAGATCTCTGAAACCGGTTATGAGTGGGCCAGAGC 930
Db 541 GAAATCAACCGCAGCGCCAGATGAGATTCTCAAGCGCGGCTATGAGCTCGGTGAAAGT 600
QY 931 CCGGTGATTTGGCGTACCACTGCGAGAGTATGAGTGGATGGCGCGGGTAGTGGATCT 990
Db 601 CCGGTGATTTGGCGTACCACTGCGAGAGTATGAGTGGATGGCGCGGGTAGTGGATCT 660
QY 991 GCGGTGATTTGGCGTACCACTGCGAGAGTATGAGTGGATGGCGCGGGTAGTGGATCT 1050

PD	28-NOV-1996.	
XX		
XX	24-MAY-1996; 96WO-JF001402.	
XX		
PR	25-MAY-1995; 95JP-00149781.	
XX	26-MAR-1996; 96JP-00094680.	
XX		
PA	(AJIN) AJINOMOTO CO INC.	
PI		
PI	Mihara Y, Utagawa T, Yamada H, Asano Y;	
XX		
XX	WPI; 1997-021215/02.	
DR	P-PSDB; AAW36462.	
XX		
PT	Efficient production of nucleoside 5'-phosphate - by reaction of a	
PT	nucleoside with a phosphoric acid donor in the presence of an acid	
PT	phosphatase.	
XX		
PS	Example 8; Page 50-51; 95pp; Japanese.	
XX		
CC	The present sequence encodes the <i>Morganella morganii</i> NCIMB 10466 acid	
CC	phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate	
CC	ester from the corresponding nucleoside when a phosphate donor, e.g. poly	
CC	- , phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH	
CC	3.0 to 5.5. The PA can be used for the economic and efficient production	
CC	of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals	
CC	and intermediates for pharmaceuticals	
XX		
SQ	Sequence 750 BP; 198 A; 194 C; 198 G; 160 T; 0 U; 0 Other;	
	Query Match 34.4%; Score 422; DB 2; Length 750;	
	Best Local Similarity 72.7%; Pred. No. 6.9e-122;	
	Matches 545; Conservative 0; Mismatches 205; Indels 0; Gaps 0	
QY	331 ATGAAAAAAGTGTTCTGGCAGTTGTTTTCGCGCATGTCTCTCTCAGSCCCTGGCG 390	
DB	1 ATGAAGAAGAATATATTATCGCGGTGCTGTCTCTACATGTTTCCCTTCGCGCTGCC 60	
QY	391 CTGTCCTCTACCGCAACGACACTACACGAAACCGGATCTCTACTACTCAAGACAGT 450	
DB	51 GCGATCCGCGGGCAACGATGCCACCACCAACGCGATTATATTCTGAAAAATGAA 120	
QY	451 GAGCCATTAAACGCTGCGCTGTGTGGCGGCAACACGCGGTGGCTCATTCGCTTT 510	
DB	121 CAGGCTATCGACAGCCTGAATCTGTACCGCCACGCGCGGAGTCGGCAGTATTCAGTTT 180	
QY	511 CTCAACCATCAGGCGCATGTATGAACAGGCGGCGCTGCTGCGCAACACCGAAGCGGTAA 570	
DB	181 TTAATGATCAGGCAATGTATGAGAAAGCCGTATGCTGCGCATACCGAGCGCGAAA 240	
QY	571 CTGCGCGGAGATGCAAACTCAGACAGTGGCGGGTGGCGAATGCTTTTCGCGCGG 630	
DB	241 CAGGCAACGCGCAGATGCTGACTCTGGCGCAGGGGGTGTGGCAACCGCATTTTCAGGGGCA 300	
QY	631 TTTGTTAGCCGATCACGAAAAAGACGCCCGCGCTGCATAAATTAATGACCAATATG 690	
DB	301 TTGCGCTATCGATTAACGAAAAAGACTCTCGAGCTGTATTAATGCTGACCAATATG 360	
QY	691 ATTGAGGACGCGGGGATCTGGCGACCGGACCGGAAAGATCACTATATGCGCATTCG 750	
DB	361 ATTGAGGATGCGGTGATCTTGCCACCGCTCCGCCAAAGAACATTATCATGCGCATCCG 420	
QY	751 CCGTTCCGTTTATGGGTTCTTACCTGTAAATACCAACGAGCAGGCAAACTGTCCAA 810	
DB	421 CCGTTTCGTTTATGCGCACAGAAACCTGTAAATACCAAGATCAGAAAAAATCTCCACC 480	
QY	811 AATGGCTCTTATCCGTCGGGCATACCTCTATTCGCTGGGCTACTCGCTGTGTGTCGCA 870	
DB	481 AACGATCTTACCGTCAGTCTATCGTCTATCGGCTGGGCAACCGCATCTGTGTGGCG 540	
QY	871 GAGATCAACCCCTCAGCGCCAGAACGAGATCTTGAACACCGCGTTATGAGCTGGGCGAGAC 930	
DB	541 GAAGTGAACCCGCAATCAGGATGCGATCTCGAAACCGGGGTATCAGCTCGGACAGAGC 600	

Qy	931	CGGGTGATTTCGGGCTACACCTGGCAGAGTGTGGATCCGCGCGGGTAGTGGGATCT	990
Db	601	CGGGTGATTTCGGGCTATCATCTGGCAGAGTGTGGATCCGCGCGGGTAGTGGGATCA	660
Qy	991	GCCTGTGTGGCGACCCCTGCATACCAACCCCGGCTTCCAGCAGCAGTTGCAGAAAGCGAAG	1050
Db	661	GCCTGTGTGGCGACATTACATTCGGATCCGGCATTTCAGCGCAGTTAGCGAAAGCCAAA	720
Qy	1051	GCCTGAATTCGCCCGCAGCATCAGAGAAATAA	1080
Db	721	CAGCAATTTGCACAAAAATCACAGAAATAA	750
RESULT 11			
AAV43045			
ID	AAV43045 standard; DNA; 750 BP.		
XX	AAV43045;		
XX	21-OCT-1998 (first entry)		
DT	DNA encoding an acid phosphatase enzyme.		
XX	Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;		
KW	intermediate; ds.		
XX	Morganella morganii.		
OS	Location/Qualifiers		
FF	Key	1..750	
FT	CDS	/*tag= a	
FT	sig_peptide	1..60	
FT	mat_peptide	61..747	
FT		/*tag= c	
XX	EP857788-A2.		
PN	12-AUG-1998.		
XX	20-NOV-1997; 97EP-00309365.		
PD	21-NOV-1996; 96JP-00311103.		
XX	18-JUN-1997; 97JP-00161674.		
PR	(AJIN) AJINOMOTO CO INC.		
XX	Mihara Y, Utagawa T, Yamada H, Asano Y;		
PI	WPI; 1998-416010/36.		
XX	P-PSDE; AAW71028.		
DR	Preparation of nucleoside 5'-phosphates comprises reacting nucleoside		
XX	with phosphate donor in presence of acid phosphatase - used as seasonings		
PT	or pharmaceutical intermediates.		
PT	Example 8; Page 30-31; 83pp; English.		
XX	The present sequence encodes an acid phosphatase enzyme. The		
CC	specification describes a method for the preparation of nucleoside 5'-		
CC	phosphate ester. The method comprises reacting a nucleoside with a		
CC	phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that		
CC	has been altered to increase its affinity for the nucleoside and/or to		
CC	increase its thermal stability, or in the presence of a microorganism		
CC	that has been transformed with recombinant DNA containing a gene coding		
CC	for such an acid phosphatase. Nucleoside 5'-phosphates are useful as		
CC	seasonings or pharmaceuticals or as intermediates for them		
XX	Sequence 750 BP; 198 A; 194 C; 198 G; 160 T; 0 U; 0 Other;		
XX	Query Match 34.4%; Score 422; DB 2; Length 750;		
XX	Best Local Similarity 72.7%; Pred. No. 6.9e-122;		

Matches 545; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 331 ATGAAAACGTTCTCCAGTTGTTGCGCATGTTCTCTCAGGCCCTGGCG 390
DB 1 ATGAGAAGAAATATATCGCGGTGTCCTCTCAGTTGTTCCCTTCGCGCTGCC 60

QY 391 CTGGTCTGCTACCGGCAACGACATACACCAAAACCGGATCTCTACTACCTCAAGAACGT 450
DB 61 GCATCCCGGGGCAACGATGACACCAACGCGGATTTATATATCTGAAAAATGAA 120

QY 451 GAAGCCATTAAAGCCTGCGCTGTTCCGCGCACCAACGCGGTGGCTCCATTGCGTTT 510
DB 121 CAGGCTATCAGACGCTGAACTGTTACCGCACCGCGGAAAGTCGCGCATTTCACTTT 180

QY 511 CTCAACGATCAGCCCATGATGACAGCGGCGCTGTCGCAACCGACCGCGGTAAAG 570
DB 181 TTAATGATCAGCAATGATGAAAGGCGGTATGCTGCGCAATACGAGCGGGA 240

QY 571 CTGCGCGGGAAGATGCAACCTGAGCAGTGGCGGGTGGCGAATGCTTTCTCCGGCG 630
DB 241 CAGGCAAGCAGATGCTGACCTGGCGCAGCGGTGTGGCAACCGCATTTTCAGGGCA 300

QY 631 TTGGTAGCCGATCACGAAAAGACGCGCCCGCGCTGCAATAAATTAAGCAATATG 690
DB 301 TTGGCTATCCGATACCGAAAAGACTCTCCGAGCTGTATTAACCTGCTGACCAATG 360

QY 691 ATTGAGGACCGGGATCTGGGACCGCGCAGCGGAAAGATCACTATATGCGCATTCGT 750
DB 361 ATTGAGGATCCGGTGTATCTGACCGCGCTCGCCAAAGCAATTAATGCGCATCCGG 420

QY 751 CCGTTCGCTTTATGGGGTCTCTACTGTAATACCAACCGAGCAGCAAACTGTCCAAA 810
DB 421 CCGTTGCGTTTACGCAAGAACCTGTATACCAAGATCAGAAAACCTCTCCACC 480

QY 811 AATGCTCTTATCCGTCGCGCATCTCTATCGGCTGGGTCTGCGCTGCTGGCA 870
DB 481 AAGCGATCTTACCGCTCAGGCTATACCTCTATCGGCTGGGCAACCGCATGCTGGCG 540

QY 871 GAGATCAACCTCAGCGCGAGACGAGATCTGAAACGCGTTATGAGTGGGCGCAGAG 930
DB 541 GAGTGAAACCGGCAATCAGATGCGATTTGAAACGCGGTTATCAGCTCGACAGC 600

QY 931 CCGGTGATTTGCGCTACCTGCGCAGATGATGCGGCGCGGTGATGCGATCT 990
DB 601 CCGGTGATTTGCGCTACCTGCGCAGATGATGCGGCGCGGTGATGCGATCT 660

QY 991 GCGTTGCGGACCTGATACCAACCGCGCTTCCAGCAGCAGTTGCAAGAGCAG 1050
DB 661 GCGCTGCGCGCATTTACATTCGATCCGCGCATTTCCAGCGCGATTTAGCGAAGCCAAA 720

QY 1051 GCGAATTCGCCAGCATCAGAAATAA 1080
DB 721 CAGGAATTCAGAAAATCAGAAATAA 750

RESULT 12
AA745012
ID AA745012 standard; DNA; 747 BP.
XX AA745012;
AC AA745012;
XX
DE 13-AUG-1997 (first entry)
XX
DE Providencia stuartii ATCC 29851 acid phosphatase DNA.
XX
KW ATCC 29851; acid phosphatase; production; nucleoside; 5'-phosphate;
KW ester; condiment; pharmaceutical; intermediate; ds.
XX
OS Providencia stuartii.
XX
FH Key Location/Qualifiers
CDS 1..747
FT /*tag= a

/product= "acid_phosphatase"

PT XX WO9637603-A1.
XX XX 28-NOV-1996.
XX XX 24-MAY-1996; 96WO-JP001402.
XX XX 25-MAY-1995; 95JP-00149781.
XX XX 26-MAR-1996; 96JP-00094680.
XX XX (AJIN) AJINOMOTO CO INC.
XX XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX XX WPI; 1997-021215/02.
XX XX P-PSDB; AAM06457.

PT Efficient production of nucleoside 5'-phosphate - by reaction of a
PT nucleoside with a phosphoric acid donor in the presence of an acid
PT phosphatase.
XX

PS Example 23; Page 63-65; 95pp; Japanese.

XX The present sequence encodes the Providencia stuartii ATCC 29851 acid
CC phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
CC -phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
CC 3.0 to 5.5. The PA can be used for the economic and efficient production
CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
CC and intermediates for pharmaceuticals
XX

XX Sequence 747 BP; 226 A; 156 C; 166 G; 199 T; 0 U; 0 Other;

Query Match 29.2%; Score 357.4; DB 2; Length 747;

Best Local Similarity 67.6%; Pred. No. 1.5e-101;
Matches 502; Conservative 0; Mismatches 241; Indels 0; Gaps 0;

QY 331 ATGAAAACGTTCTGCGCAGTTGTTGTTGCGCGAGGGCTTTGTTTCAACAGTGATTTGCG 390
DB 1 ATGAAAACGTTCTGCGCAGTTGTTGTTGCGCGAGGGCTTTGTTTCAACAGTGATTTGCG 60

QY 391 CTGTCCTCTACGCGCAAGCACATACACGAAACGCGATCTCTACTACTCAAGAACAGT 450
DB 61 GCGATCCCTCCCGCAATGATGTGCAAACTAAACCGCATCTTATTTATTTAAAAAATCA 120

QY 451 GAAGCCATTAAAGCCTGCGCTGTTGCGCGCACCAACCGCGGTGGCTCCATTGCGTTT 510
DB 121 CAGGCTATTTGATGTTTAGCGTTTATTTGCGCGCACCACTGAGTGGGCGAGTCTTTATTT 180

QY 511 CTCAACGATCAGGCGCATGTATGAAACAGGCGCGCTGCTGCGCAACACCGAAGCGGTAAAG 570
DB 181 TTAACGACCAAGCATGTATGAAAGGCGGTTTATTTGCAAAATCACTGCGGTGAGAA 240

QY 571 CTGCGCGGGAAGATGCAACCTGAGCAGTGGCGGGTGGCGAATGCTTTCTCCGGCGCG 630
DB 241 CAAGCGCTAGGATGCTGATCTGCGCTGCGGGCGGTGTTGCGAAGCGCATTTTCTGAAGCT 300

QY 631 TTTGCTAGCCGATCACCGAAAAGACGCGCCCGCGCTGCAATAAATTAAGCAATATG 690
DB 301 TTTGTTATCCCATTCGAAAAGATGCGGCTGAAATTCATTAATTCCTGCGAATATG 360

QY 691 ATTGAGGACCGGGATCTGGCGAACCGCGAGCGGAAAGATCACTATATGCGCATTCGT 750
DB 361 ATTGAGGATCCGGGATTTAGCAACTGCTCTCAGCAAGAGAAATATCATGCGCATTCGT 420

QY 751 CCGTTGCGGTTTATGGGTCTCTACCTGTAATACCAACCGAGCAGCAAACTGTCCAAA 810
DB 421 CCAITTTGCGTTCTACGGTGTGCTACCTGTAACTGTAACGAAAGATCAGGCAAAATTTCTAAG 480

QY 811 AATGCTCTTATCCGTCGCGCATCTCTATCGGCTGGGTCTGCGCTGCTGGCA 870
DB 481 AATGCTCTTATCCCTTTCTGGAACACACCGCAATTTGCTGGGCATCTGCACTCGTATGTCA 540

QY 871 GAGATCAACCTCAGCGCCAGACAGATCTGTAAACGGGTTATGAGTGGCCAGAGC 930
 DB 541 GAAATTAACCCAGAAAACAGATAAAATTTAAACGGTGGTTATGAACCTGGCCRAAGC 600
 QY 931 CGGTGATTTTCGGGTACCACTGGCAGAGTGATGTGGATGCCGCGGGTAGTGGGATCT 990
 DB 601 CGAGTCATCTGTGGTTACCAATGGCAAGTGATGTGATGCAGTCGTATCGTTGCATCG 660
 QY 991 GCCGTGTGGGACCTCGATACCAACCGGGGTTCCAGCAGCACTTGCAGAAAGGAG 1050
 DB 661 GGTGGGTAGCAACTTTACACTCCAACTCGAATTCCTAAACAGTTCAAAAAGCCAAA 720
 QY 1051 GCCGAATTCGCCAGCATCAGAA 1073
 DB 721 GACGAATTTGCTAAACTGAAAA 743

RESULT 13
 AAV43059
 ID AAV43059 standard; DNA; 747 BP.
 XX AC
 XX AC
 XX AAV43059;
 DT 21-OCT-1998 (first entry)
 XX DE DNA encoding an acid phosphatase enzyme.
 XX XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 XX KW intermediate; ds.
 XX OS Providencia stuartii.
 XX XX
 FH Key Location/Qualifiers
 FT CDS 1..747
 FT /*tag= a

EP857788-A2.
 XX 12-AUG-1998.
 XX 20-NOV-1997; 97EP-00309365.
 XX 21-NOV-1996; 96JP-00311103.
 XX 18-JUN-1997; 97CP-00161674.
 XX (AJTN) AJTNMOTO CO INC.
 XX XX
 XX Mihsara Y, Utgawa T, Yamada H, Asano Y;
 XX WP: 1998-416010/36.
 XX P-PSDB; AAV71230.
 XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.
 XX Example 23; Page 40-41; 83pp; English.

The present sequence encodes an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC that has been transformed with recombinant DNA containing a gene coding
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them

XX SQ Sequence 747 BP; 226 A; 156 C; 166 G; 199 T; 0 U; 0 Other;
 Query Match 29.2%; Score 357.4; DB 2; Length 747;
 Best Local Similarity 67.6%; Pred. No. 1.5e-101;

Matches 502; Conservative 0; Mismatches 241; Indels 0; Gaps 0;
 QY 331 ATGAAAAAGCGTGTCTGGCAGTTGTTTGTGGCGCATTTCTCTCTCAGGCCCTGGCG 390
 DB 1 ATGAAAAAATATTATAGCAGTATTTGGCAGGGGCTTTTGTTCACACAGTGTATTGCG 60
 QY 391 CTGGTCGCTACCGGCAACGACACTACACGAAACCGGATCTCTACTACTCAAGAACAGT 450
 DB 61 GCGATCCCTCCCGCAATGATGTGACAACTAAACCCGATCTTTATTTTAAAAAACTCA 120
 QY 451 GAAGCCATTAAACGCTGGCGCTGTTCGCCACACCGCGTGGGCTCCATTGGCTTT 510
 DB 121 CAGGCTATTGATAGTTTAGCGTTATTGCCGCCACACCTGAAGTGGGCGATCTATTATT 180
 QY 511 CTCAACGATCAGGCCATGTATGAAACAGGGGCGCTGTCTGGCAACACCGACCGGTAAAG 570
 DB 181 TTAACGACCAAGCGATGTATGAAAAAGGCGCTTTATTGCGAAATACTGAGCGTGAGAA 240
 QY 571 CTGGCGGGGGAAGATGCAAACTGAGCAGTGGCGGGTGGCGAATCTTCTCCGGCGG 630
 DB 241 CAAGCGCTTAGGATGCTGATTTGGCTGGGGCGGTGTTGCGAACCATTTCTGAAGCT 300
 QY 631 TTTGGTAGCCCGATCACCGAAAGACGCGCCCGCGCTGCATAAATTTACTGACCAATATG 690
 DB 301 TTTGGTTATCCCATTTACCGAAAGGATGCGCTGAAATTCATTAATTTGCTGCAATATG 360
 QY 691 ATTGAGGACCGCGGGGATCTGGCGACCCGCGAGCGCGAAAGATCACTATATGGCATTCGT 750
 DB 361 ATTGAGATGCGGGGATTTAGCAACTGCTCAGCCAAAGAGAAATACATGCGCATTCGT 420
 QY 751 CCGTTGCGGTTTTATGGGGTCTCTACTGTATATACCGAGCAGGACCAACTGTCCAAA 810
 DB 421 CCATTGCGTTCTTACCGGTGTGTACTGTAAACAGAAAGATCAGGACAAATTTATCTAAG 480
 QY 811 AATGCTCTTTATCGTCCGCGCATCTCTATCGGCTGGGCTACTCGCTGGTGTCTGGCA 870
 DB 481 AATGGCTCTTTATCTTCTGGACACCGCAATTTGGCTGGCATCTGCATCTGATTGTCA 540
 QY 871 GAGATCAACCCCTCAGCGCCAGAACGAGATCTCTCAAAACGGGTTATGAGTGGGCCAGAGC 930
 DB 541 GAAATTAACCCAGAAAACCAAGATAAAATTTAAACGGTGGTTATGAACCTGGCCRAAGC 600
 QY 931 CGGTGATTTTCGGGTACCACTGGCAGAGTGATGTGGATGCCGCGGGTAGTGGGATCT 990
 DB 601 CGAGTCATCTGTGGTTACCAATGGCAAGTGATGTGATGCAGTCGTATCGTTGCATCG 660
 QY 991 GCCGTGTGGGACCTCGATACCAACCGGGGTTCCAGCAGCACTTGCAGAAAGGAG 1050
 DB 661 GGTGGGTAGCAACTTTACACTCCAACTCGAATTCCTAAACAGTTCAAAAAGCCAAA 720
 QY 1051 GCCGAATTCGCCAGCATCAGAA 1073
 DB 721 GACGAATTTGCTAAACTGAAAA 743

RESULT 14

AAAT45009

ID AAT45009 standard; DNA; 735 BP.

XX AC

XX AAT45009;

XX AC

XX 13-AUG-1997 (first entry)

XX DT

XX DE Serratia marcescens IAM 13540 acid phosphatase DNA.

XX XX

XX KW IAM 13540; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
 XX condiment; pharmaceutical; intermediate; ds.

XX OS

XX Serratia marcescens.

XX XX

XX FH Key Location/Qualifiers

XX FT CDS 1..735

XX FT /*tag= a

Query Match 24.9%; Score 304.6; DB 2; Length 735;
Best Local Similarity 63.7%; Pred. No. 6.4e-85;
Matches 463; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 351 AGTTTGTGCGGATTTCTCTCTCAGGCCCTGGGCTGGTCTACCGGCAACGA 410
DB |||||
DB 9 AATATTATTAGCCATTAAAGCTGGCGCGGTTGACGCGAGTTTCTCTTGGCGCCAAAGA 68
QY 411 CACTACCAAGAACCGGATCTCTACTACCTCAAGACAGTGAAGCCATTAAAGCCTGGC 470
DB |||||
DB 69 TGTCACTACCCACCTGAGGTTTATTCTTCTGCAAGAAATCACAGTCCATCGACAGCCTGGC 128
QY 471 GCTGTTGGCGCCACACCGCGGCTGGGCTCCATTGGGTTTCTCAAGCATCAGGCCATGTA 530
DB |||||
DB 129 ACTATTGCCCGCGCCCGCGGATGACAGCATTTGATTTCTGTAATGACAAAGCGCAATA 188
QY 531 TGAACAGGGGCGGCTGCTCGCAACACCGAAGCGGTAAGCTGGCGCGGGAAGATCAAA 590
DB |||||
DB 189 CGAGCGCGGGAATAAGTGGCAATCTCCGCGTGCAAGCAGGCTTATGATGACGCCA 248
QY 591 CTTGAGCAGTGGCGGCTGGGAATGCTTCTCCGCGGCTTGGTAGCCCGATCACCGA 650
DB |||||
DB 249 CGTTGCGGGGAGCGGCTTGGCGCGCATTTTCCAAACGCTTTCGGCTAGAAATAGCCCA 308
QY 651 AAAAGAGCGCCCGGCTGCATAAATTTACTGACCAATATGATTGAGGAGCGCGGGATCT 710
DB |||||
DB 309 ACGGAAGCGCGGAGCTGTTTAAGCTGGTATGAAATGCGTGAAGAGCGCGGCGATTT 368
QY 711 GCGGACCGCGAGCGGGAAGATCACTATATGCGCATTCGTTCCGTTTCGCGTTTATGGGT 770
DB |||||
DB 369 GCGGACCGCGAGCGGCAAAATCACTATATGCGCATTCGCGCTTTCGCGTTTATAACGA 428
QY 771 CTCTACCTGTAATACACGAGCAGGACAAACTGTCCMAAATGCGCTTATCGGTCCG 830
DB |||||
DB 429 AGCGACCTGCGGACCGGACGAAAGACCCCTGTGAAAGACGGTTCTTACCCCTTCGG 488
QY 831 GCATACCTCTATCGGCTGGGCTACTCGGCTGGTGTGCGAGAGATCAACCTTCAGGCGCA 890
DB |||||
DB 489 CCATACCAACNTCGGCTGGCGNCCGCGCTGGTGTGCTGAATCAACCCCGCAGGCA 548
QY 891 GAACGAGATCTGAACACGCGGTTATGAGCTGGGCCAGAGCGGGTGAATTTGGGCTACCA 950
DB |||||
DB 549 GGGTGAATCTCTGACGCGGCTATGATATGGGCCAAAGCCGGTTATCTGCGGTTATCA 608
QY 951 CTGGCAGAGTGTGGATGCGCGGGGTAGTGGGATCTGCGGTTGTGGGACCCCTGCA 1010
DB |||||
DB 609 CTGGCAAGCGAGCTGACTGCGGCGGCTGCGGCGGCTGCGGCTGCGGCGGCTTGA 668
QY 1011 TACCAACCGGCGTTCAGCAGCAGTTGCAAGAGCGAGGCGCAATTCGCCCAGCATCA 1070
DB |||||
DB 669 TGGCGAACCTACCTTCGCGGCCAGCTGCAAGAGCCAAAGACGAATTCACGGCCTGAA 728
QY 1071 GAAGAAA 1077
DB |||||
DB 729 AAAGTAA 735

Search completed: June 4, 2004, 19:01:36
Job time : 416 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 19:59:11 ; Search time 432 Seconds
(without alignments)
12936.216 Million cell updates/sec

Title: US-09-807-990-1

Perfect score: 1225

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	44.6	3.6	62909	13	US-10-672-787-32
2	39.6	3.2	1830	13	US-10-672-787-32
3	37.6	3.1	1332	15	US-10-156-761-2570
4	37.6	3.1	9025608	15	US-10-156-761-2570
5	37.4	3.1	1695	13	US-10-342-887-1167
6	37.4	3.1	1695	13	US-10-172-118-1167
7	37.4	3.1	2270	15	US-10-393-590-61
8	37.4	3.1	2270	15	US-10-393-567-61
9	37.4	3.1	2270	15	US-10-394-087-61
10	37.4	3.1	2310	9	US-09-319-172-34
11	37.4	3.1	2310	9	US-09-374-298-42
12	37.4	3.1	2310	13	US-10-116-802-210
13	37	3.0	639	13	US-10-027-632-279124
14	37	3.0	639	13	US-10-027-632-279125

C 15	37	3.0	639	16	US-10-027-632-279124	Sequence 279124,
C 16	37	3.0	639	16	US-10-027-632-279125	Sequence 279125,
C 17	37	3.0	1866	9	US-09-738-626-1317	Sequence 1317, Ap
C 18	37	3.0	3309400	9	US-09-738-626-1	Sequence 1, Appl
C 19	36.8	3.0	945	16	US-10-084-846A-71	Sequence 71, Appl
C 20	36.8	3.0	59816	16	US-10-084-846A-1	Sequence 1, Appl
C 21	36.8	3.0	59816	16	US-10-084-846A-2	Sequence 2, Appl
C 22	36.8	3.0	68750	14	US-10-014-717-1	Sequence 1, Appl
C 23	36.8	3.0	71989	13	US-09-727-889-2	Sequence 2, Appl
C 24	36.4	3.0	354	15	US-10-156-761-5162	Sequence 5162, Ap
C 25	36.4	3.0	669	16	US-10-260-238-5254	Sequence 5254, Ap
C 26	36.4	3.0	9025608	15	US-10-156-761-1	Sequence 1, Appl
C 27	36.2	3.0	2229	15	US-10-156-761-5567	Sequence 6567, Ap
C 28	36	2.9	867	15	US-10-156-761-1437	Sequence 1437, Ap
C 29	36	2.9	2000	9	US-09-887-576-333	Sequence 333, App
C 30	35.8	2.9	732	13	US-10-282-122A-14920	Sequence 14920, A
C 31	35.8	2.9	1017	13	US-10-440-503-29	Sequence 29, Appl
C 32	35.8	2.9	1017	13	US-10-461-925-29	Sequence 29, Appl
C 33	35.8	2.9	1017	15	US-10-146-772-29	Sequence 29, Appl
C 34	35.8	2.9	1017	16	US-10-241-742-29	Sequence 29, Appl
C 35	35.8	2.9	1017	16	US-10-440-523-29	Sequence 29, Appl
C 36	35.6	2.9	888	9	US-09-974-300-1129	Sequence 1129, Ap
C 37	35.2	2.9	536	17	US-10-338-110-119	Sequence 119, App
C 38	35	2.9	586	15	US-10-029-386-12315	Sequence 12315, A
C 39	35	2.9	645	15	US-10-207-655-417	Sequence 417, App
C 40	34.6	2.8	802	15	US-10-184-644-312	Sequence 312, App
C 41	34.6	2.8	802	15	US-10-184-634-312	Sequence 312, App
C 42	34.4	2.8	1404	13	US-10-282-122A-26411	Sequence 26411, A
C 43	34.4	2.8	1407	13	US-10-282-122A-28207	Sequence 28207, A
C 44	34.4	2.8	1971	16	US-10-369-493-39994	Sequence 39994, A
C 45	34.4	2.8	1995	16	US-10-369-493-39628	Sequence 39628, A

ALIGNMENTS

RESULT 1

US-10-672-787-32/c
; Sequence 32, Application US/10672787
; Publication No. US20040067554A1
; GENERAL INFORMATION:
; APPLICANT: LAGACE, Robert, E.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BERG, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: ELITRA.025C1
; CURRENT APPLICATION NUMBER: US/10/672,787
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 09/596,002
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 62909
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-10-672-787-32

Query Match 3.6%; Score 44.6; DB 13; Length 62909;

Best Local Similarity 53.8%; Pred. No. 0.011;

Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 793 CAGGACAACTGTCACAAAATGGCTTTATTCCTCGGGGATACCTTATTCGGTGGGCT 852

Db 40121 CAAAGCAGAGAAAGAAAATTCATCTTATCCAAAGTGGGATACCTCCAAATGGTTTGGT 40062

QY 853 ACTGGCTGGTGTGGCAGAGATCAACCTTCAGCGCCAGACGAGATCCTGAAACGGGT 912

Db 40061 CAAAGCGGTTGTGATGGGATGGCAATTCCTTGAGCGAGGTCAAGAGATATCTCTCGTGA 40002

QY 913 TATGAGCTGGCGCAGAGCGGGTATTTGGCGTACCACTGGCAGAGTGAT 963

Db 40001 TTCCAGTATGGAGAAAGCCGAGTCATTTGGGTGTGATTTTCCACAGAT 39951

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RESULT 2
US-10-282-122A-25435
; Sequence 25435, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Chlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25435
; LENGTH: 1833
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25435

Query Match      3.2%; Score 39.6; DB 13; Length 1830;
Best Local Similarity 48.9%; Pred. No. 0.064;
Matches 136; Conservative 0; Mismatches 139; Indels 3; Gaps 1;

QY 390 GCTGTCCTACCGCAACGACACTACACGAAACCGGATCTCTACTACTCTCAAGAACAG 449
DB 225 GGTGCTCTCGCCGAGGACGAGACCGGAGCTGTGGAGCTCTCGACCTGACCTACGG 284
QY 450 TGAAGCCATTAAACGCTGGCGCTGTTCGCGCCACACCGCGGTGGGTCCATTGCGGT 509
DB 285 CGAGGACGAGGACACCGAGGAGGACCTGCAGACGCGCGCGGTGGTACCGTATGGG 344
QY 510 TCTCAACATCGGCCATGTATACAGGGGCGCTGTGCGCAACGACGACGACGGTAA 569
DB 345 TCACGTGACACCGGTAGACGCGGCTGCTGGACACGATCCGTAGGGCCAACTCGGGA 404
QY 570 GCTGCGCGGGAAGATGCAAACTCAGCAGTGGCGGGGT---GGCGAATGCTTTCTCCGG 626
DB 405 GCGGAGCGCGGCGATCACCACACATCGGCGCTACAGGTGACCGTGCAGACGA 464
QY 627 CCGCTTTGTAGCCCGGATCACCGAAAAAGACGCCCGG 664

RESULT 3
US-10-156-761-2570
; Sequence 2570, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2570
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-10-156-761-2570

Query Match      3.1%; Score 37.6; DB 15; Length 1332;
Best Local Similarity 51.8%; Pred. No. 0.26;
Matches 85; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 857 CGCTGCTGTCGACGAGATCAACCTCAGCGCCAGAACGAGATCTCTGAACGCGTTATG 916
DB 479 CGATGGCGCTGACCGCGAGACATCGCGTACAGAACGGCTTCGACCGTTTCGCGCCG 538
QY 917 AGCTGGCGCAGAGCGCGGTGATTTCGGGCTACCATCGCAGAGTGTGATGCGCGC 976
DB 539 AGGTCTACCGGCTGCGGTGCGGTACCGCTACCGTGTGCTACCGCGCCGAGAACGCG 598
QY 977 GGTAGTGGGATCTGCGCTGTGGCGACCTCATACCAACCG 1020
DB 599 GTGCCGAGGCGCTCGCCGCGGATCGACATGATCAACAGCAG 642

RESULT 4
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
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; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 3.1%; Score 37.6; DB 15; Length 9025608;
Best Local Similarity 51.8%; Pred. No. 63; Mismatches 79; Indels 0; Gaps 0;
Matches 85; Conservative 0;

QY 857 CGCTGGTGTGGCAGAGATCAACCTTCAGCGCCAGAAACGAGATCTTGAAACGCGGTATG 916
Db 3175941 CGATGGCGCTGACCGGAGACATGCGGTACAGAAACGCGTTCGGACCGTTCCGCCCG 3176000

QY 917 AGCTGGGCGAGACCGCGGTGATTTGCGGTACACATGCGCAGAGTATGTGGATGCGGCGC 976
Db 3176001 AGGTACCGGGTGGCGGTGGCGTACCGGTACCGTGGTACCGGCGCGGAGAAACGCG 3176060

QY 977 GGGTAGTGGGATCTCCGTTGTGGCGACCTCATACCAACCG 1020
Db 3176061 GTGCCGAGGCTCCGCCAGCGGATGACATGATCAACAGCAG 3176104

RESULT 5
US-10-342-887-1167
; Sequence 1167, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1167
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: XM 005554
; DATABASE ENTRY DATE: 2001-06-18
US-10-342-887-1167

Query Match 3.1%; Score 37.4; DB 13; Length 1695;
Best Local Similarity 49.2%; Pred. No. 0.35;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 881 CTCAGCGCCAGAACGAGATCTTGAAACGCGGTATGAGTGGCCAGAGCCGGTGATTT 940
Db 1145 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACACGTCGAAGAAGCAGT 1204

QY 941 GCGGTACCACTGGCAGAGTGTGATGCGCGGGGTAGTGGATCTGCCGTTGTGG 1000
Db 1205 GCGCAACCTGCGAGCGGCCCATCTGCTGATGCTGAGCAGCGTGGGGAGATGGCCCTCAAGG 1264

QY 1001 CGACCTCTCATACCAACCGCGGTTCACAGCAGAGTTGCAGAAAGCGAAGGCCAATTGC 1060
Db 1265 ATGCCAAGAACAGCTGTGGAAGGCTGGAGGATGCCCTGCAGAAAGGCCAAGCAGGACCTGG 1324

QY 1061 CCCAGCATCAGAAGAATA 1079
Db 1325 CCCGGCTGCTGAAGGAGTA 1343

RESULT 7
US-10-393-590-61
; Sequence 61, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 61
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: human
US-10-393-590-61
```

```

Db 1325 CCCGGCTGCTGAAGGAGTA 1343

RESULT 6
US-10-172-118-1167
; Sequence 1167, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1167
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: XM 005554
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1167

Query Match 3.1%; Score 37.4; DB 13; Length 1695;
Best Local Similarity 49.2%; Pred. No. 0.35;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 881 CTCAGCGCCAGAACGAGATCTTGAAACGCGGTATGAGTGGCCAGAGCCGGTGATTT 940
Db 1145 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACACGTCGAAGAAGCAGT 1204

QY 941 GCGGTACCACTGGCAGAGTGTGATGCGCGGGGTAGTGGATCTGCCGTTGTGG 1000
Db 1205 GCGCAACCTGCGAGCGGCCCATCTGCTGATGCTGAGCAGCGTGGGGAGATGGCCCTCAAGG 1264

QY 1001 CGACCTCTCATACCAACCGCGGTTCACAGCAGAGTTGCAGAAAGCGAAGGCCAATTGC 1060
Db 1265 ATGCCAAGAACAGCTGTGGAAGGCTGGAGGATGCCCTGCAGAAAGGCCAAGCAGGACCTGG 1324

QY 1061 CCCAGCATCAGAAGAATA 1079
Db 1325 CCCGGCTGCTGAAGGAGTA 1343

RESULT 7
US-10-393-590-61
; Sequence 61, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 61
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: human
US-10-393-590-61
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Query Match 3.1%; Score 37.4; DB 15; Length 2270;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 881 CTCAGCGCCAGAACGAGATCTCTGAACCGCGTTATGAGCTGGCCGAGCGCGGTGATT 940
DB 1193 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACCAAGTCAAGAAGCAGT 1252
QY 941 GCGGCTACCACTGGCAGAGTGTGATGTCGCCGCGGTAGTGGATCTGCCGTTGTGG 1000
DB 1253 GCGCCAACTGACGCGCGCCATTCTGATCTGAGCAGCGTGGGAGAGGCCCTCAAGG 1312
QY 1001 CGACCTGCTATCAACCGCGCTTCAGCAGCAGTTCGAGAAAGCGAAGCGCAATTTCG 1060
DB 1313 ATGCCAAGAACAGCTGGAGGCTGGAGGATGCCCTGCGAAGGCCCAAGCAGGACCTGG 1372
QY 1061 CCCAGCATCAGAAAGATA 1079
DB 1373 CCGGCTGCTGAAGGAGTA 1391

RESULT 8

US-10-393-567-61
; Sequence 61, Application US/10393567
; Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; TYPE: DNA
; ORGANISM: human
US-10-393-567-61
Query Match 3.1%; Score 37.4; DB 15; Length 2270;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 881 CTCAGCGCCAGAACGAGATCTCTGAACCGCGTTATGAGCTGGCCGAGCGCGGTGATT 940
DB 1193 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACCAAGTCAAGAAGCAGT 1252
QY 941 GCGGCTACCACTGGCAGAGTGTGATGTCGCCGCGGTAGTGGATCTGCCGTTGTGG 1000
DB 1253 GCGCCAACTGACGCGCGCCATTCTGATCTGAGCAGCGTGGGAGAGGCCCTCAAGG 1312
QY 1001 CGACCTGCTATCAACCGCGCTTCAGCAGCAGTTCGAGAAAGCGAAGCGCAATTTCG 1060
DB 1313 ATGCCAAGAACAGCTGGAGGCTGGAGGATGCCCTGCGAAGGCCCAAGCAGGACCTGG 1372
QY 1061 CCCAGCATCAGAAAGATA 1079
DB 1373 CCGGCTGCTGAAGGAGTA 1391

RESULT 9

US-10-394-087-61
; Sequence 61, Application US/10394087
; Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: Jatkoe, Tim
; TITLE OF INVENTION: SELECTION OF MARKERS
; FILE REFERENCE: CDS 265 US NP
; CURRENT APPLICATION NUMBER: US/10/394,087
; CURRENT FILING DATE: 2003-03-21

; PRIOR APPLICATION NUMBER: 60/368,790
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; TYPE: DNA
; ORGANISM: human
US-10-394-087-61

Query Match 3.1%; Score 37.4; DB 15; Length 2270;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 881 CTCAGCGCCAGAACGAGATCTCTGAACCGCGTTATGAGCTGGCCGAGCGCGGTGATT 940
DB 1193 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACCAAGTCAAGAAGCAGT 1252
QY 941 GCGGCTACCACTGGCAGAGTGTGATGTCGCCGCGGTAGTGGATCTGCCGTTGTGG 1000
DB 1253 GCGCCAACTGACGCGCGCCATTCTGATCTGAGCAGCGTGGGAGAGGCCCTCAAGG 1312
QY 1001 CGACCTGCTATCAACCGCGCTTCAGCAGCAGTTCGAGAAAGCGAAGCGCAATTTCG 1060
DB 1313 ATGCCAAGAACAGCTGGAGGCTGGAGGATGCCCTGCGAAGGCCCAAGCAGGACCTGG 1372
QY 1061 CCCAGCATCAGAAAGATA 1079
DB 1373 CCGGCTGCTGAAGGAGTA 1391

RESULT 10

US-09-919-172-34
; Sequence 34, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 008513.49
; NAME/KEY: unsure
; LOCATION: 2307
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-34

Query Match 3.1%; Score 37.4; DB 9; Length 2310;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 881 CTCAGCGCCAGAACGAGATCTCTGAACCGCGTTATGAGCTGGCCGAGCGCGGTGATT 940
DB 1203 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACCAAGTCAAGAAGCAGT 1262
QY 941 GCGGCTACCACTGGCAGAGTGTGATGTCGCCGCGGTAGTGGATCTGCCGTTGTGG 1000
DB 1263 GCGCCAACTGACGCGCGCCATTCTGATCTGAGCAGCGTGGGAGAGGCCCTCAAGG 1322
QY 1001 CGACCTGCTATCAACCGCGCTTCAGCAGCAGTTCGAGAAAGCGAAGCGCAATTTCG 1060
DB 1323 ATGCCAAGAACAGCTGGAGGCTGGAGGATGCCCTGCGAAGGCCCAAGCAGGACCTGG 1382

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; OTHER INFORMATION: Incyte ID No: 008513.49
; NAME/KEY: unsure
; LOCATION: 2307
; OTHER INFORMATION: a, t, c, g, or other
US-10-116-802-210

Query Match      3.1%; Score 37.4; DB 13; Length 2310;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1061 CCCAGCATCAGAGAAATA 1079
    |||||
Db 1383 CCCGCTCTGAAGGAGTA 1401

RESULT 11
US-09-974-298-42
; Sequence 42, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chug, Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 42
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 008513.49
; NAME/KEY: unsure
; LOCATION: 2307
; OTHER INFORMATION: a, t, c, g, or other
US-09-974-298-42

Query Match      3.1%; Score 37.4; DB 9; Length 2310;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 881 CTCAGCGCCAGAACGAGATCTCTGAACCGCGTATAGCTGGGCCAGAGCCGGGTGATTT 940
    |||||
Db 1203 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACACGTCGAAGACGT 1262

QY 941 GCGGCTACCACTGGCAGAGTGTGATGCGCGCGGGTAGTGGGATCTGCCGTGTGG 1000
    |||||
Db 1263 GCGCAACCTGCGAGCGCGCCATGCTGTGATGCTGAGCAGCGTGGGAGATGCCCTCAAGG 1322

QY 1001 CGACCCCTGATACCAACCGCGGTTCCAGCAGAGTTCGAGAAAGCGAGCCGATTCG 1060
    |||||
Db 1323 ATGCCAAGAACCAAGCTGGGAAGGCTGGAGGATGCCCTGCAGAGGCCCAAGCAGGACCTGG 1382

QY 1061 CCCAGCATCAGAGAAATA 1079
    |||||
Db 1383 CCCGCTCTGAAGGAGTA 1401

RESULT 13
US-10-027-632-279124/c
; Sequence 279124, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279124
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION:
US-10-027-632-279124

Query Match      3.0%; Score 37; DB 13; Length 639;
Best Local Similarity 58.7%; Pred. No. 0.26;
Matches 64; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 496 GCTCCATTGCGTTTCTCAACGATCAGCGCATGTATGAACAGGGGGCGCTGCTGCGCAAC 555
    |||||
Db 593 GCTGGAGTGGAGTTTCTACATGGAGGCGCTGCAGCTTCAGGGTTGGCTGCTGCCCTC 534

QY 556 ACCGAACGCGGTAAGCTGGCGGGAAGATGCAACCTGAGCAGTGGCG 604
    |||||
Db 533 CCCCAAGGAGCTCAGATGCTTAGACAGCAGGCGACACAGCAGTGGT 485

; OTHER INFORMATION: Incyte ID No: 008513.49
; NAME/KEY: unsure
; LOCATION: 2307
; OTHER INFORMATION: a, t, c, g, or other
US-10-116-802-210

Query Match      3.1%; Score 37.4; DB 13; Length 2310;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1061 CCCAGCATCAGAGAAATA 1079
    |||||
Db 1383 CCCGCTCTGAAGGAGTA 1401

RESULT 11
US-09-974-298-42
; Sequence 42, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chug, Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 42
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 008513.49
; NAME/KEY: unsure
; LOCATION: 2307
; OTHER INFORMATION: a, t, c, g, or other
US-09-974-298-42

Query Match      3.1%; Score 37.4; DB 9; Length 2310;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 881 CTCAGCGCCAGAACGAGATCTCTGAACCGCGTATAGCTGGGCCAGAGCCGGGTGATTT 940
    |||||
Db 1203 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACACGTCGAAGACGT 1262

QY 941 GCGGCTACCACTGGCAGAGTGTGATGCGCGCGGGTAGTGGGATCTGCCGTGTGG 1000
    |||||
Db 1263 GCGCAACCTGCGAGCGCGCCATGCTGTGATGCTGAGCAGCGTGGGAGATGCCCTCAAGG 1322

QY 1001 CGACCCCTGATACCAACCGCGGTTCCAGCAGAGTTCGAGAAAGCGAGCCGATTCG 1060
    |||||
Db 1323 ATGCCAAGAACCAAGCTGGGAAGGCTGGAGGATGCCCTGCAGAGGCCCAAGCAGGACCTGG 1382

QY 1061 CCCAGCATCAGAGAAATA 1079
    |||||
Db 1383 CCCGCTCTGAAGGAGTA 1401

RESULT 12
US-10-116-802-210
; Sequence 210, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 210
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
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RESULT 14
US-10-027-632-279125/c
; Sequence 279125, Application US/10027632
; Publication No. US2002019837A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279125
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-279125
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```
Query Match      3.0%; Score 37; DB 13; Length 639;
Best Local Similarity 58.7%; Pred. No. 0.26;
Matches 64; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 496 GGCCTCCATTGGCGTTTCTCAACGATCAGGCCATGTATGAACAGGGCGCGCTGCTGGGCAAC 555
    |||||
DB 593 GGCCTGAGTGGGAGTTTCTACATGAGGCGCTGCAGCTTCAGGGTTGGCTGCTGCCCTC 534

QY 556 ACCGAACGGGTAAGCTGCGCGGAGATGCAAACTGAGCAGTGGCG 604
    |||||
DB 533 CCCCAAGGAGTTCAGATGCTTAGACAGCAGGACACACAGCAGTGGTG 485
```

```
RESULT 15
US-10-027-632-279124/c
; Sequence 279124, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 279124
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-279124

Query Match      3.0%; Score 37; DB 16; Length 639;
Best Local Similarity 58.7%; Pred. No. 0.26;
Matches 64; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 496 GGCCTCCATTGGCGTTTCTCAACGATCAGGCCATGTATGAACAGGGCGCGCTGCTGGGCAAC 555
    |||||
DB 593 GGCCTGAGTGGGAGTTTCTACATGAGGCGCTGCAGCTTCAGGGTTGGCTGCTGCCCTC 534

QY 556 ACCGAACGGGTAAGCTGCGCGGAGATGCAAACTGAGCAGTGGCG 604
    |||||
DB 533 CCCCAAGGAGTTCAGATGCTTAGACAGCAGGACACACAGCAGTGGTG 485

Search completed: June 4, 2004, 21:45:45
Job time : 451 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: June 4, 2004, 18:46:46 ; Search time 2464 Seconds
(Without alignments)
14846.255 Million cell updates/sec

Title: US-09-807-990-1
Perfect score: 1225
Sequence: 1 ctgcaggcgaaagcaatgt.....taagatcatgtgcggttaac 1225

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513283 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_hic.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_hic.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estoc.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_mam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_pig.*
- 27: em_gss_vil.*
- 28: gb_ges1.*
- 29: gb_ges2.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	60.2	4.9	827	BZ571331	BZ571331: msh2_1837
C 2	51.4	4.2	793	BZ571419	BZ571419 msh2_1877
C 3	41.6	3.4	1002	BZ566646	BZ566646 pace2-164
4	41	3.3	1201	BX381961	BX381961 BX381961

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	40.8	3.3	1101	29	CNS006BP
C 6	40.8	3.3	1201	13	BX381961
7	40.2	3.3	1201	13	BX360624
8	40	3.3	577	14	CF267657
9	39.8	3.2	940	28	BZ578090
C 10	39.4	3.2	1115	10	BE796660
C 11	39.2	3.2	837	12	BM045366
C 12	39.2	3.2	907	13	BX425011
C 13	38.2	3.1	704	13	BQ815676
14	38.2	3.1	1201	13	BX446497
15	38	3.1	698	29	CT735352
16	37.8	3.1	406	14	CF486989
C 17	37.8	3.1	548	14	CD552112
C 18	37.8	3.1	667	28	BZ714274
C 19	37.8	3.1	685	12	B1731187
20	37.8	3.1	708	12	BG335783
21	37.8	3.1	767	29	CG124285
22	37.8	3.1	805	29	CG058565
C 23	37.8	3.1	857	28	BZ976081
C 24	37.8	3.1	859	12	BG676301
C 25	37.8	3.1	875	29	CG208072
C 26	37.8	3.1	3997	29	AY400436
27	37.6	3.1	546	14	CF861045
C 28	37.6	3.1	564	12	B1392452
29	37.6	3.1	646	10	BE584929
30	37.6	3.1	730	12	B1085396
C 31	37.6	3.1	971	12	BM016444
C 32	37.6	3.1	1201	13	BX460099
C 33	37.4	3.1	213	12	BG991567
34	37.4	3.1	370	9	AV046877
35	37.4	3.1	499	10	BE514697
36	37.4	3.1	504	12	BM688482
37	37.4	3.1	513	12	BM706530
38	37.4	3.1	515	13	BX284006
39	37.4	3.1	549	12	BG679897
40	37.4	3.1	554	12	BM018419
41	37.4	3.1	568	12	BM686861
42	37.4	3.1	570	12	BG676692
43	37.4	3.1	584	12	BG680375
44	37.4	3.1	593	10	BE272392
45	37.4	3.1	650	12	BG676653

ALIGNMENTS

RESULT 1
BZ571331/c

LOCUS
DEFINITION

ACCESSION
VERSION

KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BZ571331
msh2_1837.Y2 msh Pseudomonas aeruginosa genomic clone msh2_1837,
Genomic survey sequence.

BZ571331
BZ571331.1 GI:27206392
GSS.

Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

1 (bases 1 to 827)

Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.

Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library

J. Bacteriol. (2002) in press
Contact: Chris K. Raymond
Genome Center

University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244

Email: craymond@u.washington.edu
Class: stougun.
Location/Qualifiers

FEATURES

	source	1. .827 /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="WSH" /db_xref="taxon:287" /clone="msh2_1817" /notes="Environmental isolate. Whole genomic shotgun library."	
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	Query Match	4.9%; Score 60.2; DB 28; Length 827;	
	Best Local Similarity	55.5%; Pred. No. 1.6e-05;	
	Matches	116; Conservative 0; Mismatches 93; Indels 0; Gaps 0;	
QY	817	TCTATCCGTCGGGCATACCTTATCGGTGGGCTACTCGCGTGTCGTGGCAGAGATC	876
DB	376	TCTATCCGTCGGGCATACCTTATCGGTGGGCTACTCGCGTGTCGTGGCAGATCTG	318
QY	877	AACCCCTCAGCGCCAGAACAGAGATCCCTGAACACGGGTTATGAGCTGGGCCAGAGCCGGGTG	936
DB	317	GTCCCGGAGCATCACGATGGCTTCTTCGCCCGCCGCGAGAGGATGCGCAGAGCCGTGTG	258
QY	937	ATTGCGGCTACCCTGGCAGAGTAGTGATGTCGCCGCGGGTAGTGGGATCTGCCGTT	996
DB	257	CTGGCCGGGTGCACTTCCCGACGACCTGGAAGCGGGCAGACCGCGCGCGCGCTG	198
QY	997	GTGGCGGACC 1005	
DB	197	GTGGCGGACC 189	
	RESULT 3		
	BZ566646	1002 bp DNA linear GSS 17-DEC-2002	
	LOCUS	Pacs2-164_5502.y2 pacs2-164 Pseudomonas aeruginosa genomic clone	
	DEFINITION	Pacs2-164_5502, genomic survey sequence.	
	ACCESSION	BZ566646	
	VERSION	BZ566646.1 GI:27196581	
	KEYWORDS	GSS.	
	SOURCE	Pseudomonas aeruginosa	
	ORGANISM	Pseudomonas aeruginosa	
	REFERENCE	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	
	AUTHORS	Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library	
	JOURNAL	J. Bacteriol. (2002) In press	
	COMMENT	Contact: Chris K. Raymond Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, USA Tel: 2062216954 Fax: 2066857244 Email: craymond@u.washington.edu Class: shotgun.	
	FEATURES	Location/Qualifiers	
	source	1. .1002 /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /db_xref="taxon:287" /clone="pacs2-164_5502" /clone_lib="pacs2-164" /notes="clinical isolate 2-164 Whole genomic shotgun library."	
	ORIGIN		
	Query Match	3.4%; Score 41.6; DB 28; Length 1002;	
	Best Local Similarity	54.6%; Pred. No. 3.5;	
	Matches	83; Conservative 0; Mismatches 69; Indels 0; Gaps 0;	
QY	817	TCTATCCGTCGGGCATACCTTATCGGTGGGCTACTCGCGTGTCGTGGCAGAGATC	876
DB	391	TCTATCCGTCGGGCATACCTTATCGGTGGGCTACTCGCGTGTCGTGGCAGATCTG	450
QY	877	AACCCCTCAGCGCCAGAACAGAGATCCCTGAACACGGGTTATGAGCTGGGCCAGAGCCGGGTG	936
DB	451	GTCCCGGAGCATCACGATGGCTTCTTCGCCCGCCGCGAGAGGATGCGCAGAGCCGGGTG	510
QY	937	ATTGCGGCTACCCTGGCAGAGTAGTGATGTCGCCGCGGGTAGTGGGATCTGCCGTT	968
DB	511	CTGGCGGCGTGCACITTTCCCGACGACCTGGA 542	

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RESULT 4
BX381961
LOCUS
DEFINITION
BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI072YF05 3-PRIME, mRNA sequence.
BX381961
VERSION
BX381961.1 GI:30453007
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI072CC03NP1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI072YF05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES
source
Query Match 3.3%; Score 41; DB 13; Length 1201;
Best Local Similarity 3.8%; Pred. No. 5.7;
Matches 27; Conservative 249; Mismatches 434; Indels 0; Gaps 0;
QY 173 APTGCTGGCCCTGTTGTGCAACAAACGCTTTATTGTGTAATTTTGTGACGTATATC 232
Eb 399 ANNNNNKMMNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNN 458
QY 233 AGGTTTAAAGCAACCTGTGTGGGCTATATCTGCAACCTGTTGATATTAAGCAACTCT 292
Db 459 KKKNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNN 518
QY 293 TCACTCAGCGAATTAAACGCCAGTAAAGGTATACGCATGCAAAAAACGTTTCTGGCAG 352
Db 519 KMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNN 578
QY 353 TTTGTTTTCGCGATTGTTCTTCTCAGCGCTGGCGTGTGTCGTACCGGCAACGACA 412
Db 579 KKKKKKKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNN 638
QY 413 CTACACAGAAACGGATCTCTACTACTCAAGACAGTGAAGCCATTACAGCCTGGCG 472
Db 639 KKKNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNN 698
QY 473 TGTTCGCGCCACACCGCGGGTGGGTCCTCATTTGCGTTTCTCAACGATCAGGCGCATGATG 532
Db 699 NNNKNNNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNN 758
QY 533 AACAGGGCGCGCTGTGCGCAACACCGAAGCGGTAAAGCTGGCGGCGGAAGATGCAAAAC 592
Db 759 MNNNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNNKNNNN 818
QY 593 TGAGCAGTGGCGGGTGGGAATGCTTTTCTCGGCGCGCTTTTGTAGCCCGCATCACGAA 652
Db 819 CKMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNNKMMNN 878
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QY 653 AAGACGCCGCGGCTGCATATAATTAAGCAATATGATTAGAGACGCGGGGATCTGG 712
Db 879 MCAMCMKMMKNNMMKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNN 938
QY 713 CGACCCCGCAGCGGAGAAAGATCACTATATGCGCAATTCGTTCGCTGGCGTTTATGGGTCT 772
Db 939 MVKKKAMNNBKCVKMMKMKCKCKKVMKBNKCAKCKKNNKCMVKVKMMCMCDKCMCKKX 998
QY 773 CTACTCTGTATACACCGAGCAGCAGCAAACTGCTCCAAAATATGGCTCTTATCCGTCGCGGC 832
Db 999 MKKVCCKKKMMNNMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMK 1058
QY 833 ATACTCTATCGGCTGGGCTACTGCGTGTGCTGGTGAGAGATCAACCT 882
Db 1059 KMSKMMKMMKVKCKMBBCKMSKGGCMCKGCTGVCNNSCCMBSK 1108
CNS006BP 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR13018 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL064052
VERSION
AL064052.1 GI:4944232
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
FEATURES
source
1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR13018"
/clone_lib="RPCI-98"
/note="end : TET3"
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ORIGIN

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Query Match 3.3%; Score 40.8; DB 29; Length 1101;
Best Local Similarity 17.9%; Pred. No. 6.2;
Matches 53; Conservative 119; Mismatches 124; Indels 0; Gaps 0;
QY 411 CACTACCAAGAACCGGATCTCTACTACCTCAAGAACAGTGAAGCCATTACACCTGGC 470
Db 789 MACGAAAMVAASAAVVAARVMSAGSSSSAAARACGAASVAVVSSSSAACACGCSAAS 848
QY 471 GCTGTTGGCGCACACCGCGGCTGGGCTCCATTTGCTTCTCAACGATCAGCCATGTA 530
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D5 849 ASAAVAASMAASAAACARSVSAASSSSSSSSSSSSSSVVAVASASSVSAASVVKSA 908
QY 531 TGAACAGGGCGCTGCTGCGCAACACCGACGGGTAGCTGCGCGCGGAAGTGCAG 590
D5 909 AAAASSSSASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 968
QY 591 CTGAGCAGTGGCGGGTGGCGAATGCTTCTCCGGCGCGTTTGGTAGCCGATCACCGA 650
D5 969 SGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1028
QY 651 AAAAGAGCGCCCGCGCTGCGCAATTAATCTACCAATATGATGAGGAGCGCGGG 706
D5 1029 SAAAVAAASWGAASASASASASASASASASASASASASASASASASASASASAS 1084

RESULT 6
LOCUS BX381961 1201 bp mRNA linear EST 08-MAY-2003
DEFINITION BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION BX381961
VERSION BX381961.1 GI:30453007
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1072CC03NPL.
FEATURES
Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
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/note="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 3.3%; Score 40.8; DB 13; Length 1201;
Best Local Similarity 3.4%; Pred. No. 6.4;
Matches 19; Conservative 179; Mismatches 353; Indels 0; Gaps 0;

QY 51 TAAGGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 110
D5 969 KVAKKBMGGKMKMKMGVNYKTKTMMMBKXKXKXKXKXKXKXKXKXKXKXKXKXKX 910
QY 111 ACCTGAGCGCGCGGGTCCCGCGCGCTTTTATGCGGCTCGGTGAGGAGCG 170
D5 909 MKKGGKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 850
QY 171 TTATCTGCTGCGCTGTTGTCGCAACAACTTTTATGTTGTAATTTTGTGAGGTATA 230
D5 849 NMVTKGKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 790
QY 231 TCAGGTTTAAAGCACCTGTCGCTCATCTGGCAACCTGTTGATATTAAGCAACACT 290
D5 789 SKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 730

```

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QY 291 CTTCACTCAGCAATTAACAGCACAGTAAGTATACGCATGAAAGAAACGTTCTTGGC 350
D5 729 KNNANNNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 670
QY 351 AGTTTGTTCGCGCATTTCTCTCTCAGGCCCTGGCGCTGGCTACCGGCAACGA 410
D5 669 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 610
QY 411 CACTACCAAGAAACCGGATCTCTACTACTCAAGAACAGTGAAGCCATTAACAGCCTGC 470
D5 609 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 550
QY 471 GCTGTTCGCGCACACCGCGGTGGCTCCATTCGCTTCTCAAGCATGACGCGCATGTA 530
D5 549 KKKKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 490
QY 531 TGAACAGGGCGCTGCTGCGCAACACCGACGGGTAGCTGCGCGCGGAAGTGCAG 590
D5 489 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 430
QY 591 CTTGAGCAGTG 601
D5 429 NKMMNNNNNNNG 419

RESULT 7
LOCUS BX360624 1221 bp mRNA linear EST 05-MAY-2003
DEFINITION BX360624 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION BX360624
VERSION BX360624.1 GI:30376452
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4982.i
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1072CF03NPL.
FEATURES
Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1072YJ05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 3.3%; Score 40.2; DB 13; Length 1201;
Best Local Similarity 11.4%; Pred. No. 9.6;
Matches 36; Conservative 153; Mismatches 126; Indels 0; Gaps 0;

QY 356 GTTTTGGCGCATTTCTCTCTCAGGCCCTGGCGCTGGCTACCGCAACGACTA 415
D5 887 KTTTWTATAAATTTAAWSBSBSBSBSBSBSBSBSBSBSBSBSBSBSBSBSBSBS 946
QY 416 CCAGAAACCGGATCTCTACTACTCAAGAACAGTGAAGCCATTAAACAGCCTGGCGCTGT 475

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```

RESULT 12
BX425011/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

FEATURES
source
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CL0BA007ZB02"
    /tissue_type="PLACENTA"
    /clone_lib="Homo sapiens PLACENTA"
    /notes="Vector: pCMVSPORT.6; 1st strand cDNA was primed
    with a NotI-oligo(dT) primer. Five prime end enriched,
    double-strand cDNA was digested with Not I and cloned into
    the Not I and EcoRV sites of the pCMVSPORT 6 vector.
    Library was not normalized."

ORIGIN
Query Match      3.2%; Score 39.2; DB 13; Length 907;
Best Local Similarity 43.5%; Pred. No. 16;
Matches 93; Conservative 16; Mismatches 105; Indels 0; Gaps 0;

QY      126  GGGGTCCCCGGCGCGCTTTTATGGGCGCTCGGTGAGGAGCGGTATCTGTGGCCCT 185
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      350  KGGTYCCCCCCCCCTCTTTTITTTGGGGGGGGGGKBBKAAKKTTGGTGTITTT 291

QY      186  GTTTGTGCAACAACCGTTTATGTGTAAATTTTGTGACGTATACAGTTTITTAAGCA 245
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Db      290  TTTTITTTTTCACCCCCCYTTTTTTTTTTTTTTTGGGGMSCCCCYTTTTTWTCCCC 231

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Db      170  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 137

RESULT 13
BQ815676
LOCUS
DEFINITION
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SOURCE
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REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

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    with a NotI-oligo(dT) primer. Five prime end enriched,
    double-strand cDNA was digested with Not I and cloned into
    the Not I and EcoRV sites of the pCMVSPORT 6 vector.
    Library was not normalized."

ORIGIN
Query Match      3.2%; Score 39.2; DB 13; Length 907;
Best Local Similarity 43.5%; Pred. No. 16;
Matches 93; Conservative 16; Mismatches 105; Indels 0; Gaps 0;

QY      126  GGGGTCCCCGGCGCGCTTTTATGGGCGCTCGGTGAGGAGCGGTATCTGTGGCCCT 185
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QY      246  CCCTGTGGCGCTCATCTGCGCACTGTTGATTAATTAAGCAACACTCTTCACTCAGCGAAT 305
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Db      170  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 137

RESULT 13
BQ815676
LOCUS
DEFINITION
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KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

FEATURES
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    with a NotI-oligo(dT) primer. Five prime end enriched,
    double-strand cDNA was digested with Not I and cloned into
    the Not I and EcoRV sites of the pCMVSPORT 6 vector.
    Library was not normalized."

ORIGIN
Query Match      3.2%; Score 39.2; DB 13; Length 907;
Best Local Similarity 43.5%; Pred. No. 16;
Matches 93; Conservative 16; Mismatches 105; Indels 0; Gaps 0;

QY      126  GGGGTCCCCGGCGCGCTTTTATGGGCGCTCGGTGAGGAGCGGTATCTGTGGCCCT 185
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QY      246  CCCTGTGGCGCTCATCTGCGCACTGTTGATTAATTAAGCAACACTCTTCACTCAGCGAAT 305
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Db      170  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 137


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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8860.f
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue, Genoscope sequence ID : CLOB009ZE10RP1.
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double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

FEATURES
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Best Local Similarity 40.7%; Pred. No. 35;
Matches 46; Conservative 25; Mismatches 42; Indels 0; Gaps 0;

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Qy 170 GTTATCTCGCGCTGTTCTGCAACAAAGCTTTTATGTAATTTTGT 222
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RESULT 15
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DEFINITION genomic survey sequence.
ACCESSION CC735352
VERSION CC735352.1 GI:32158289
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 698)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, J.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Unpublished (2002)
Other GSSs: OG0UB85TH
Contact: Cathy Whitelaw
TI08
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
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Location/Qualifiers

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ORIGIN
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Best Local Similarity 48.6%; Pred. No. 32;
Matches 104; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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Qy 573 GCGCGCGGAGATGCAACCTGAGCAGTGGGGGGTGGCGAATGCTTTTCGGGCGGTT 632
Db 149 CGACCGGACGGTGAAGTCGTGTCGTAGACGGGTAGCGGCAGTCGTCGGCGGGGAGGC 208

Qy 633 TGGTAGCCCGATCACCGAAAAGAGCCCGCGCGCTGCATATAATTACTGACCAATATGAT 692
Db 209 TGGCGGCGAGGTGCGCCGAAGCGCGCGCGCGCGCGCGCTTCTCCACCCACCGCGCT 268

Qy 693 TGAGGACCGCGGGATCTGGCGACCGCGCGCGCG 726
Db 269 GCAGCGGCTGCTCGACCTTGACACCCAGAGCG 302

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 18:49:36 ; Search time 85 Seconds
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Title: US-09-807-990-1

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Gapop 10.0 , Gapext 1.3

Searched: 682709 seqs, 277475446 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	750	61.2	750	4	US-09-727-578-6
5	514.6	42.0	762	4	US-09-489-039A-762
6	507	41.4	747	3	US-08-750-145A-19
7	507	41.4	747	3	US-08-975-698A-23
8	507	41.4	747	3	US-09-417-090-23
9	507	41.4	747	4	US-09-727-578-23
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11	493.4	40.3	747	3	US-08-975-698A-25
12	493.4	40.3	747	3	US-09-417-090-25
13	493.4	40.3	747	4	US-09-727-578-25
14	422	34.4	747	3	US-08-750-145A-2
15	422	34.4	750	3	US-08-975-698A-2
16	422	34.4	750	3	US-09-417-090-2
17	422	34.4	750	4	US-09-727-578-2
18	357.4	29.2	747	3	US-08-750-145A-17
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20	357.4	29.2	747	4	US-09-417-090-21
21	357.4	29.2	747	4	US-09-727-578-21
22	304.6	24.9	735	3	US-08-750-145A-23
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25	304.6	24.9	735	4	US-09-727-578-27
26	85.4	7.0	756	1	US-07-717-332D-1
27	60.8	5.0	1287	4	US-09-489-039A-3770

28	60.2	4.9	762	4	US-09-252-991A-11386	Sequence 11986, A
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30	44.6	3.6	2832	4	US-09-540-236-1538	Sequence 1538, Ap
31	44.6	3.6	62909	4	US-09-596-202-32	Sequence 32, Appl
32	37.4	3.1	2310	4	US-09-919-172-34	Sequence 34, Appl
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43	36.4	3.0	4411529	3	US-09-103-840A-1	Sequence 2, Appli
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45	35.6	2.9	832	4	US-09-621-976-2813	Sequence 2813, Ap

ALIGNMENTS

RESULT 1

US-08-750-145A-9
: Sequence 9, Application US/08750145A
: Patent No. 6010851
: GENERAL INFORMATION:
: APPLICANT: MIHARA, Yasuhiro
: APPLICANT: UTAGAWA, Takashi
: APPLICANT: YAMADA, Hideaki
: APPLICANT: ASANO, Yasuhisa
: TITLE OF INVENTION: Method for Producing Nucleoside-5'-
: TITLE OF INVENTION: Phosphate Ester
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
: STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/750,145A
: FILING DATE: 01-JAN-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-149781
: FILING DATE: 05-May-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 8-094680
: FILING DATE: 26-Mar-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: NORMAN F. OBLON
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-413-3000
: TELEFAX: 703-413-2220
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 750 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO

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Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 511 CTCAACGATCAGGCCATGTATGAACAGGGGGCGCTGTGCGCAACACCGAACCGGTAAG 570
Db 181 CTCAACGATCAGGCCATGTATGAACAGGGGGCGCTGTGCGCAACACCGAACCGGTAAG 240

QY 571 CTGGCGCGGAAGATGAAACCTGAGCAGTGGCGGTGGCGAATGTTTCTCGCGCG 630
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QY 691 ATTGAGACCGCGGGATCTGGGACCGCGCAGCGCGAAGATCACTATATGCGATTCGT 750
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RESULT 2
US-08-975-698A-6
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; Sequence 6, Application US/08975698A
; Patent No. 6015697
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIKA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,698A
; FILING DATE: 21-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0855-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 750 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
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; LOCATION: 1..54
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; NAME/KEY: mat_peptide
; LOCATION: 55..747
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US-08-975-698A-6

Query Match
Best Local Similarity 61.2%; Score 750; DB 3; Length 750;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 ATGAAAAACGTTCTGGCAGTTTGTTCGCGCATTTGTTCTCTCTCAGGCCCTGGCG 390
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QY 391 CTGGTCCTACCGCCACGACATACACGAAACCGGATCTCTACTACCTCAAGAACAGT 450
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QY 451 GAGGCCATTACAGCCCTGGCGCTGTTCGCGCCACCGCGGTGGGCTCCATTGCGTTT 510
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691	ATTGAGGACCGCGGGATCTGGCGACCCGACGCGCGAAAGATCACTATATGGGCATTCGT	750	QY
361	ATTGAGGACCGCGGGATCTGGCGACCCGACGCGCGAAAGATCACTATATGGGCATTCGT	420	DB
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RESULT 3

US-09-417-090-6
Sequence 6, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
UTAGAWA, TAKASHI
YAMADA, HIDEAKI
ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-Nov-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F

QY 931 CGGGTGAATTTGGGCTACCACTGGCAGAGTATGGATCCGCGGGTAGTGGGATCT 390
 Db 601 CGGGTGAATTTGGGCTACCACTGGCAGAGTATGGATCCGCGGGTAGTGGGATCT 660
 QY 991 GCGGTGTGGCGACCCCTGCATACCAACCCGGCGTTCAGCAGCAGTTCAGAAAGCGAAG 1050
 Db 661 GCGGTGTGGCGACCCCTGCATACCAACCCGGCGTTCAGCAGCAGTTCAGAAAGCGAAG 720
 QY 1051 GCCGAATTCGCCAGCATCAGAGAAATAA 1080
 Db 721 GCCGAATTCGCCAGCATCAGAGAAATAA 750

RESULT 4
 US-09-727-578-6
 ; Sequence 6, Application US/09727578
 ; Patent No. 6355472
 ; GENERAL INFORMATION:
 ; APPLICANT: MIHARA, YASUHIRO
 ; APPLICANT: UTAGAWA, TAKASHI
 ; APPLICANT: YAMADA, HIDEAKI
 ; APPLICANT: ASANO, YASUHIRO
 ; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
 ; TITLE OF INVENTION: ESTER
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/727,578
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/975,698
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 0010-0885-0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-3000
 ; TELEFAX: (703) 413-2220
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 750 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: genomic DNA
 ; HYDROTHERMAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Escherichia blattae
 ; STRAIN: JCM 1650
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..747
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 1..54
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: 55..747
 ; US-09-727-578-6

Query Match 61.2%; Score 750; DB 4; Length 750;
 Best Local Similarity 100.0%; Pred. No. 1.2e-239;
 Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 331 ATGAAAAACGTGTCTTGGCAGTTTGTTCGCCGATCTCTCTTCAGGCCCCGCG 390
 Db 1 ATGAAAAACGTGTCTTGGCAGTTTGTTCGCCGATCTCTCTTCAGGCCCCGCG 60
 QY 391 CTGTCGCTACCGGCAACGACACTACACGAAACCGGATCTCTACTACTCTCAAGAACAGT 450
 Db 61 CTGTCGCTACCGGCAACGACACTACACGAAACCGGATCTCTACTACTCTCAAGAACAGT 120
 QY 451 GAAGCCATTAAACAGCTGGCGCTGTTCGCCGACCAACCGCGGGTGGGCTCATTCGCTTT 510
 Db 121 GAAGCCATTAAACAGCTGGCGCTGTTCGCCGACCAACCGCGGGTGGGCTCATTCGCTTT 180
 QY 511 CTCACGATCAGGCGCATGTATGAACAGGGGCGCTGTTCGCCGACCAACCGCGGGTAAAG 570
 Db 181 CTCACGATCAGGCGCATGTATGAACAGGGGCGCTGTTCGCCGACCAACCGCGGGTAAAG 240
 QY 571 CTGCGCGGGAAGATGCAACCTGAGCAGTGTGGCGGGTGGGGAATGCTTTCTCGCGCGG 630
 Db 241 CTGCGCGGGAAGATGCAACCTGAGCAGTGTGGCGGGTGGGGAATGCTTTCTTCGCGCGG 300
 QY 631 TTTGGTAGCCCGATCACCGAAAAAGACGCCCGCGGCTTGCATTAATTTACTGACCAATATG 690
 Db 301 TTTGGTAGCCCGATCACCGAAAAAGACGCCCGCGGCTTGCATTAATTTACTGACCAATATG 360
 QY 691 ATTGAGGACGCGGGGATCTGGCGACCGCGGAGGAGATCCTATATGGCATTCCT 750
 Db 361 ATTGAGGACGCGGGGATCTGGCGACCGCGGAGGAGATCCTATATGGCATTCCT 420
 QY 751 CCGTTTCGGGTTTATGGGCTCTCTACTGTATATACCGGAGCAGGACAACTGTCAAA 810
 Db 421 CCGTTTCGGGTTTATGGGCTCTCTACTGTATATACCGGAGCAGGACAACTGTCAAA 480
 QY 811 AATGGCTTTATTCGCTCGGCGATCCTCTATGGCTGGCTACTCGGCTGGCTGGCA 870
 Db 481 AATGGCTTTATTCGCTCGGCGATCCTCTATGGCTGGCTACTCGGCTGGCTGGCA 540
 QY 871 GAGATCAACCTCAGCGCCAGAACGAGATCTGAAACCGGTTATGAGCTGGGCCAGAGC 930
 Db 541 GAGATCAACCTCAGCGCCAGAACGAGATCTGAAACCGGTTATGAGCTGGGCCAGAGC 600
 QY 931 CCGGTGATTTCGGCTACCACTGGCAGATGATGAGTGGCGGGGTATGAGATCT 990
 Db 601 CCGGTGATTTCGGCTACCACTGGCAGATGATGAGTGGCGGGGTATGAGATCT 660
 QY 991 GCGGTGGGACCCCTGCATACCAACCGCGGTTCCAGCAGCAGTTCAGAAAGCGAAG 1050
 Db 661 GCGGTGGGACCCCTGCATACCAACCGCGGTTCCAGCAGCAGTTCAGAAAGCGAAG 720
 QY 1051 GCCGAATTCGCCAGCATCAGAGAAATAA 1080
 Db 721 GCCGAATTCGCCAGCATCAGAGAAATAA 750

RESULT 5
 US-09-489-039A-762
 ; Sequence 762, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2799-2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 762

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; LENGTH: 762
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-762

Query Match 42.0%; Score 514.6; DB 4; Length 762;
Best Local Similarity 79.8%; Pred. No. 3.8e-161;
Matches 607; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 317 GTAAAGTATACGATGAAAAACGTTCTGGCAGTTTGTTCGCGCATGTTCTT 376
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 377 CTGAGGCTTGGCTGGTCTACGCGACACACTACCAAGAACCGGATCTTACT 436
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 TTAACGCTTGTCTGTGTTCCCGCGGAACGATGTCACCAAGCCGCTTACT 121
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 437 ACCTCAAGACAGTGAAGCCATTAAACGCTTGGCGCTTTCGCCGCCACCGCGGTG 496
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 122 ATCTGACCAATGCCAGGCCATCGACAGCTTGGCGCTTTCGCCACCAACCGCGGTG 181
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 497 GCTCCATGCTTCTTCAACGATCAGGCATGTATGACAGGGGCGCTTGGCACA 556
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 182 GCAGTATCGCATTTTAAACGATCAGGCGATGTATGACAAAGAGCTTGTCTGCGCA 241
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 557 CCGAACGCGTAACTGCGCGGGAAGATGCAACCTGAGCAGTGGCGGTGGCGAATG 616
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 242 CCGAGCGCGGAAGCTGGCGCGCAGGAGTGCACCTCAGCGGCGCGGTGGCAAG 301
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 617 CTTTCTCGCGCGCTTGTGAGCCGATCAGCAAAAGACCGCCCGCTGCAATAAT 676
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 302 CTTTCTCAGCGCTTGTGTCGCGATACCGAGAAAGACGCGCGCAGCTTCAAAAC 361
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 677 TACTGACCAATATGATTGAGACGCGCGGATCTGGCAGCGCGGGAAGATCACT 736
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 362 TGCTGACCAATATGATTGAGACGCGCGGACCTGGCGACCGCGAAGAAAGAAAT 421
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 737 ATATGCGCATTCGTCGCTTATGGGCTTCTACCTGTAATACACCGAGCAGG 796
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 422 ACATGCGCATTCGCGCTTGTGTCGCTTATGGGCTTCACTTGCACACCGAGCAG 481
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 797 ACAAAGTCTCAAAATGCTTATCGCTCGGGCATACTCTACCGCTGGGTACTG 856
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 482 ACAGCTGCGGAACGCGCTTACCGTTCGGGCACTACCTTATCGCTGGCGCACG 541
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 857 CGTGTGCTGCGCAGATCAACCTCTAGCGCGCAGACGAGATCTGAAACGCGTTATG 916
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 542 CCTGTGCTGCGGAGATCAACCGCGACGCGCAAAACGAAATTTTGAAGCGCGTATG 601
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 917 AGCTGGCGCAGCGCGGTGATTTCGCGCTACCACTGGCAGAGTATGATGTCGCGC 976
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 602 AGCTGCGCAGAGCGCGGTGATCTCGGCTATCATCTGGCAGAGCATGTCATGCGGCG 661
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 977 GGGTATGGGATCTCGCTTGGCGACCTGCATACCAACCGCGCTTCCAGAGCAGT 1036
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 662 GCATGCTGCGCTCGCGGTGTCGTAGCTGCACCAACCGCGCTTCCAGAGCAGT 721
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1037 TGCAGAAAGCGAAGCGCAATTCGCCAGCATCAGAGAA 1077
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 722 TGCAGAAAGCGAAGATGAATTCGGGAAAGGCGAGAGTAA 762
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 6

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US-08-750-145A-19
; Sequence 19, Application US/08750145A
; Patent No. 6010851
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: UTAGAWA, Takashi
; APPLICANT: YAMADA, Hideaki
; APPLICANT: ASANO, Yasuhisa
; TITLE OF INVENTION: Method for Producing Nucleoside-5'-
; TITLE OF INVENTION: Phosphate Ester

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; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, XAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,145A
; FILING DATE: 01-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-149781
; FILING DATE: 05-May-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-094680
; FILING DATE: 26-Mar-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: NORMAN F. OBLON
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 747 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterobacter aerogenes
; STRAIN: IFO 12010
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..744
; US-08-750-145A-19

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Query Match 41.4%; Score 507; DB 3; Length 747;
Best Local Similarity 79.9%; Pred. No. 1.3e-158;
Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 331 ATGAAAAACGTTGTTCTGGCAGTTTGTTCGCGCATGTTCTTCTCAGGCCCTGGCG 390
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QY 1 ATGAAAAAGCGGTTCTCGCCCTCGCCTCGCGCAGCTGTTTTCGTTAAOGCTTCGCG 60
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 391 CTGTGTGCTACCGGCAACGACACTACCAAGAACCGGATCTCTACCTCAGAACAGT 450
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CTGTGCTCTCGCGCAATGATGCAACCAACCGGATCTCTATATCTGAAAAATGCA 120
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 451 GAAGCCATTACAGCTGCGGCTGTTGCGCCACACCGCGCTGGCTCCATTGGCGTT 510
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CAGGGCATCATAGTCTGGCGCTGTTGCGCGCGCGCGAGTGGGAGTGGGAGCATCGCAT 180
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 511 CTCAAGCATCAGCCCATGATGAACAGGGCGCGCTGCTGCGCAACACCGAGCGGTAG 570
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 TTAACGATCAGCGCATGTATGAAAGGACGCTGTTGGCAATACCGAACGTCGCAAG 240
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 571 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGCTGGCGATGCTTCTTCGGGCG 630
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 CTGGGCGCTGAAGATGCTAACCTGAGCGCGCGCGCTGCGGAATGCTTCTCCAGCGCT 300
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 631 TTGTGTAGCCCATCAGCGAAGAGCGCCCGCGCTGCATAAATTTACTGACCAATATG 690
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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301 TTTGGTTCCGCCATCACCGAAGAGCGCGCGAGTTACATAAGCTGCTGACAAATATG 360
691 ATTGAGGAGCGCGGATCTGGCGACCCGCGAGCGGAGAGATCACTATATGCGCATTCGT 750
361 ATTGAGGATCGCGGATCTGGCGACCCGCGAGCGGAGAGAAATATATGCGCATTCG 420
751 CGGTTGCGTTTATGGGCTCTTACCTGCTATACCAACCGAGCAGCAAACTGTCAAA 810
421 CGGTTGCGTTTACGGGCTTTACCTGCTATACCAACCGAGCGGAGCAAGCTGTCAAA 480
811 AATGGCTCTTATCCGCTCGCGGATACCTCTATCCGCTGGGCTACTCGGCTGGTGGCA 870
481 AACGATCTTACCTTCGCGGCACTACTCTATCGGTTGGGCAACCGCGCTGGTGGCG 540
871 GAGATCAACCTTCAGCGCCAGAACGAGATCTCTGAACCGGCTTATGAGCTGGGCGAGGC 930
541 GAGATCAATCCGCGAGCGGCAACGAAATCTCAACCGCGGCTTATGAATGGGCGAAGC 600
931 CGGCTGATTTGGGCTACCACTGGCAGAGTATGATGGATCGCGCGGCTAGTGGGATCT 990
601 CGGCTTATCTGGGCTATCATTTGGCAGCGATGTCGATCGCGCGGAGTAGTGGGCTCG 660
991 GCGGTTGTCGCGACCTGCAATACCAACCGCGGCTTCAGCAGCAGTTGCAAGAGCGAAG 1050
661 GCGGTTGTCGCGACCTGCAATACCAACCGCGGCTTCAGCAGCAGTTGCAAGAGCGAAG 720
1051 GCGGTTGTCGCGACCTGCAATACCAACCGCGGCTTCAGCAGCAGTTGCAAGAGCGAAG 1077
721 GATGAATTCGCAAAACGCAAGTAA 747

RESULT 7
US-08-975-698A-23
; Sequence 23, Application US/08975698A
; Patent No. 6015697
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,698A
; FILING DATE: 21-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 747 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
US-08-975-698A-23
Query Match 41.4%; Score 507; DB 3; Length 747;
Best Local Similarity 79.9%; Pred. No. 1.3e-158; Indels 0; Gaps 0;
Matches 597; Conservative
331 ATGAAAAAGCGTCTCTGGCAGTTTGTTCGCGCATTTGTTCTCTCTCAGGCCCTGGCG 390
Db 1 ATGAAAAAGCGGTTTCTGGCCCTCTGCTCGCAGCGCTGTTTCGTTAAGCGTTTCGG 60
391 CTGGTCTCTACCGGCAACGACATACCAAGAAACCGGATCTCTACTACCTCAAGAACTG 450
Db 61 CTGGTCTCTCGCGCAATGATGCAACCAACCGGATCTCTATTATCTGAAAAATGCA 120
451 GAAGCCATTAACAGCTCTGGCGCTGTTGCGCGCACCGCGGCTGGCTCCATTGCGTT 510
Db 121 CAGGCCATCGATAGTCTGGCGCTGTTGCGCGCGCGCGGAGTTGGCAGCATCGCAT 180
511 CTCAGCGTCAAGCCTGATGAAACAGGCGCGCTGCTGGCGCAACCGCAACCGGCTAAG 570
Db 181 TTAAAGCTCAGCGGATGTAAGAAAGAGCGCTGTTGGCAATACCGAACGTTGGCAAG 240
571 CTGGCGCGGAGATGCAACCTGAGCAGTGGGCGGCTGGCGGATGCTTCTCGCGCGCG 630
Db 241 CTGGCGGCTGAAGATGCTAACTGAGCGCGCGCGCTGCGGAATGCTTCTCCAGCGCT 300
631 TTTGGTAGCCCGATCACGGAAGAGCGCGCGCTGCTGATAAATTACTGACCAATATG 690
Db 301 TTTGGTTTCGCCCATCACCGAAAAAGCGCGCGCGGTTTACATAAGCTCTGCAAAATG 360
691 ATTGAGCAGCGCGGATCTGGCGACCGCGCGGAGAGATCTATATGCGGATTCGT 750
Db 361 ATTGAGGATGCGCGGATCTGGCGACCGCGCGGAGAGAGAAATATATGCGATTCGC 420
751 CGGTTGCGTTTATGGGCTCTTACCTGTAATACCGCGAGCAGGACAACTGTCGAAA 810
Db 421 CGGTTGCGTTTCTACGCGGTTTCAACCTGTAACACTACCGAGCAGCAAGCTGCGAAA 480
811 AATGGCTCTTATCGGCTCGGCGATCTCTATCGGCTGGGCTACTGCGCTGTTGCTGGCA 870
Db 481 AACGATCTTACCTTTCGCGCATACCTCTATCGGTTGGGCAACCGCGCTGTTGCGG 540
871 GAGATCAACCTTCAGCGCGCAGACGAGATCTGAAAACCGGTTATGAGCTGGGCGAGAC 930
Db 541 GAGATCAATTCGCGAGCGGCAACGAAATTCGAAACCGGCTATGAAATGGCGGAAAGC 600
931 CGGCTGATTTGCGGCTACCATCTGCGAGATGATGTCGCGCGGCTGGGCTGGGATCT 990
Db 601 CGGCTTATCTCGGCTATCATTTGGCAGCGGATGTCGATGCGCGCGGATAGTTCGGCTG 660
991 GCGGTTGTCGCGACCTGCAATACCAACCGCGGCTTCAGCAGCAGTTGCAAGAGCGAAG 1050
Db 661 GCGGTTGTCGCGACCTGCAATACCAACCGCGGCTTCAGCAGCAGTTGCAAGAGCGAAG 720
1051 GCCGAATTCGCGCGATGCAAGAA 1077
Db 721 GATGAATTCGCAAAACGCAAGTAA 747
RESULT 8
US-09-417-090-23
; Sequence 23, Application US/09417090
; Patent No. 6207435
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO

UTAGAWA, TAKASHI
YAMADA, HIDEAKI
ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 1201C
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-417-090-23

Query Match 41.4%; Score 507; DB 3; Length 747;
Best Local Similarity 79.9%; Pred. No. 1.3e-158;
Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 331 ATGAAAAAGGTTCTGGCAGTTGTTTGGCGCATTTCTTCTTCAGGCGCTGGG 390
DB 1 ATGAAAAAGGTTCTGGCAGTTGTTTGGCGCATTTCTTCTTCAGGCGCTGGG 60
QY 391 CTGGTTCGCTACCGGCAACGACACTACGAAACCGGATCTCTACTACAGAACAGT 450
DB 61 CTGGTTCGCTACCGGCAACGACACTACGAAACCGGATCTCTACTACAGAACAGT 120
QY 451 GAAGCATTACAGCTGGCGCTGTTCGCGCACCAACCGCGGTGGCTCCATTGGTTT 510
DB 121 CAGGCCATCGATAGTCTGCGCTGTTCGCGCACCAACCGGATCTCTACTACAGAACAGT 180
QY 511 CTCACGATCAGCGCATGTATCAACAGGGCGCGCTCTCGCAACACCGAGCGGTAAG 570
DB 181 TTAACGATCAGCGCATGTATGAGAAAGACCGCTGTTCGCGCAATACCGAGTGCAAG 240
QY 571 CTGGCGGGGAAAGATGCAAACTGAGCAGTGGCGGGTGGGAAATGCTTTCTCCGCGGG 630
DB 241 CTGGCGGCTGAAGATGCTAACTGAGCGCGCGGGTGGCGAAATGCTTTCTCCAGCGCT 300

QY 631 TTTCGTAGCCCGATCACCGAAAAAGAGCCCGCGGCTGCATAAATTACTGACCAATATG 690
DB 301 TTTCGTAGCCCGATCACCGAAAAAGAGCCCGCGGCTGCATAAATTACTGACCAATATG 360
QY 691 ATTGAGGAGCGCGGGATCTGGCGACCGCGAGCGGGAAGATCACTATATGCGATTGCT 750
DB 361 ATTGAGGATGCGCGGATCTGGCGACCGCGAGCGGGAAGAAATATATGCGATTGCT 420
QY 751 CGGTTGCGTTTATGGGCTCTCTACCTGTGAATACACCGAGCAGGACAAACTGTCCAAA 810
DB 421 CCGTTTGGGTTCTACGCGGTTTCACTGTGAATACACCGAGCAGGACAACTGTCTGAAA 480
QY 811 AATGGCTCTTATCGGTCCGGGCATACCTCTATGGCTGGGCTACTGCGCTGTGTGGCA 870
DB 481 AACGGATCTTACCTTTCGGGCGCATACCTCTATGGCTGGGCAACCGCGCTACTGCGG 540
QY 871 GAGATCAACCTCAGCGCGCAGAACGAGATCTTGAACCGGTTATGAGCTGGGCGAGAGC 930
DB 541 GAGATCAATCGCGAGCGGCAAAACGAAATCTCAACCGCGGCTATGAATGGGCGGAAAGC 600
QY 931 CGGGTGATTTGCGGCTACCACTGGCAGAGTGTATGGATGCCCGCGGCTAGTGGGATCT 990
DB 601 CGGGTTATCTGCGGCTATCATTTGGCAGAGCATGTGATGCGCGCGGATAGTGGCTCG 660
QY 991 GCCGTTGTGGGACCTCGCATACCAACCGCGGTTCCAGCAGCAGTTGCAGAAAGCGAAG 1050
DB 661 CGGGTTGTGGGACCTCGCATACCAACCGCGGTTCCAGCAGCAGTTGCAGAAAGCGAAG 720
QY 1051 GCGGAATTGCGGCGCAGCATCAGAGAAA 1077
DB 721 GATGAATTGCGCAAAACGCGAAGTAA 747

RESULT 9
US-09-727-578-23
Sequence 23, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 23:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 747 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterobacter aerogenes
; STRAIN: IFO 12010
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..744
;
US-09-727-578-23

Query Match 41.4%; Score 507; DB 4; Length 747;
Best Local Similarity 79.9%; Pred. No. 1.3e-158;
Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 331 ATGAAAAAGCGTCTGGCAGTTGTTTGGCCGATGTTCTCTCAGGCCCTGGCG 390
DB 1 ATGAAAAAGCGGTTCTGCGCTCTGCTCGCAGCGCTGTTTCGGTTAAGCTTCGG 60

QY 391 CTGCTGCTACCGCAACGACACTACCACGAAACCGGATCTCTACTACCTCAAGAACAGT 450
DB 61 CTGCTGCTCGCGGCANTGATGCAACCAACACCGGATCTCTATCTATCTGAAAAATGCA 120

QY 451 GAAGCCATTAAACAGCTGGCGCTGTTTCGCCGACCAACCGGGTGGGCTCATTCGCTTT 510
DB 121 CAGGCCATCGATAGTCTGGCGCTGTTTCGCCGCGCGCGGAGTTGGCAGCATCGCATTC 180

QY 511 CTGACGATCAGGCGCATGTATGACAGGCGGCTGCTGGCCACACCGACGCGGTAAAG 570
DB 181 TTAACACATCAGGCGATGTATGAAAGGAGCGGCTGTTGCCAATTCGGAACGTGGCAG 240

QY 571 CTGCGCGCGAAGATGAAACCTCAGCACTGCGCGGCTGGCGAATGCTTTCCGGCGCG 630
DB 241 CTGCGCGCTGAGATGTCTACCTGAGCGCGCGCGGCTGGCGAATGCTTTCCAGCGCT 300

QY 631 TTTGGTAGCCGATCAGCGAAAAAGCGCCCGCGGCTGCGAATTAATCTACGACATATG 690
DB 301 TTTGGTTGCGCCATCAGCGAAAAAGCGCGCGGCTGACATAGCTCTGACAAATATG 360

QY 691 ATTGAGGACGCGGGATCTGGCAGCGCGGCGGAGGATCTATATGCGATTGCT 750
DB 361 ATTGAGGATGCGCGGATCTGGCAGCGCGGCGGAGGAGAAATATATGCGATTGCG 420

QY 751 CCGTTGCGGTTTATGGGGTCTCTACCTGTATATACCAACGAGCAGGACAACTGTCCAAA 810
DB 421 CCGTTGCGGTTCTAGCGGTTTCAACCTGTAACTACCTAGCAGCAGCAAGCTGTGAAA 480

QY 811 AATGGCTTTATCGTCCGGCATCTCTATCGCTGGGCTACTCGCTGGTGTGCGCA 870
DB 481 AACGGATCTTACCTTCCGGCATCTCTATCGGTTGGGCAACCGCGCTGTACTGGCG 540

QY 871 GAGATCAACCTCAGCGCCAGAACGAGATCTCTGAAACGCGTTATGAGCTGGCGCAGAGC 930
DB 541 GAGATCAATCCGACGCGGAAACGAAATCTCTAAACGCGGCTATGAATTGGCGGAAAGC 600

QY 931 CGGGTAGTTTCGGCTACCACTGGCAGAGTATGTGATGCGCGGGGTATGCGGATCT 990
DB 601 CGGGTTAICTCGGCTATCATTTGGCAGAGCGATGTCGATCGGCGCGGATATGCGCTCG 660

QY 991 GCGGTTGGCGACCTTGATACCAACCGCGGTTCCAGCAGCATGTCAGAAAGCGGAG 1050
DB 661 GCGGTTGGCGACCTTGATACCAACCGCGGTTCCAGCAGCATGTCAGAAAGCGGAG 720

QY 1051 GCGGAATTCGCCAGCATCAGAAAGAA 1077
DB 721 GATGAATTCGCCAAACGCGAAGTAA 747
```

```

;
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 747 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Klebsiella planticola
; STRAIN: IFO 14939
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..747
; US-08-975-698A-25
;
; Query Match 40.3%; Score 493.4; DB 3; Length 747;
; Best Local Similarity 79.0%; Pred No. 4.4e-154;
; Matches 587; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
;
QY 331 ATGAAAACGTTCTCGCAGTTCTGTTTGGCCGCAATGTTCTCTCTCTCAGGCGCTGGCG 390
Db 1 ATGAAAAGCGTTACTGCGCTTGGCTTGGCAGCTCTTTTCAGTTAGCGCCTTTGGG 60
QY 391 CTGTGCTGACGGCAACGACACTACACGAAACCGGATCTCTACTACCTCAAGAACAGT 450
Db 61 CTGTTCCTCGCGCGCAATGATGCCACCAACGACCGGATCTCTACTATCTGAAAATGCC 120
QY 451 GAAGCATTAAACAGCTGCGCTGTTGGCCGCAACACCGCGCGTGGGCTCCATTTGCGTTT 510
Db 121 CAGGCAATTGACAGCTGCGCTGTTGCCACCGCGCGGAAAGTGGGAGCATTTGGTTT 180
QY 511 CTCAACGATAGCGCATGATGAAACAGGGGCGCTGCTGCGCAACACCGAACGCGGTAAG 570
Db 181 TTAACGATCAGCGATGATGAGAAAGCGCTGCTGCGCGCCACCGCGCGGCAAG 240
QY 571 CTGGCGCGGAGATGCAACCTGAGCAGTGGCGGGTGGCGAATGCTTTCTCCGCGCGG 630
Db 241 TTGGCGCGGAGATGCGCAACCTGAGCGCGGGTGGCGTGGCGCAACGCTTCTCCGCGCA 300
QY 631 TTTGCTAGCGCGCATCACCGAAAAGACGCGCGCGCTCATATAAATTACTGACCAATATG 690
Db 301 TTCGCTCCCGCATCAGCGAAAAGACGCGCGCGCTGCACAACTGCTCACCACATG 360
QY 691 ATTGAGGACGCGCGGATCTGGCGACCGCGGCAAGATCCTATATGCGCATTCGT 750
Db 361 ATTGAGGACGCGCGGATCTGGCGACCGCGGCAAGATCCTATATGCGCATTCGT 420
QY 751 CGGTTGCGGTTTATGGGCTCTCTACTGTAATACCAACGAGAGATCCTATATGCGCATTC 810
Db 421 CGGTTGCGCTTCTACGCGGTGTCACCTGTAATACCAACGAGAGATCCTATATGCGCATTC 480
QY 811 AATGGCTCTTATCCGTCGCGGATCTCTATGCGGTGGGCTACTGCGTGGTGGTGGCA 870
Db 481 AACGCTCTTACCTTCCGACACACCTCTATGCGTGGGCGACCGCTGCTGCTGCGCC 540
QY 871 GAGATCAACCTCAGCGCAGAACGAGATCTTGAAACCGGGTATGATGCTGGCGCAGAGC 930
Db 541 GAAATCAACCGCAGCGCAGAACGAGATCTTGAAACCGGGTATGATGCTGGCGCAGAGT 600
QY 931 CGGTTGCGGTTTATGGGCTCTCTACTGTAATACCAACGAGAGATCCTATATGCGCATTC 990
Db 601 CGGTTGCGCTTCTACGCGGTGTCACCTGTAATACCAACGAGAGATCCTATATGCGCATTC 660
QY 991 GCCGTTGTCGCGACCTCTGATACCAACCGCGGCTTCCAGCAGCAGTTCGAGAAACGAG 1050
Db 661 CGCGTTGTTGCAACCTCTGATACCAACCGCGGCTTCCAGCAGCAGTTCGAGAAACGAG 720
;
; US-08-975-698A-25
; Sequence 25, Application US/08975698A
; Patent No. 6015697
;
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSES: OHLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,698A
; FILING DATE: 21-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OHLON, NORMAN F
; REGISTRATION NUMBER: 24,618
;

```

QY 1051 GCCGAATTCGCCAGCATCAGAA 1073
DB 721 GACGAGTTTGGGAAACAGCAGAA 743

RESULT 12
US-09-417-090-25
Sequence 25, Application US/09417090
Patent No. 635472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
UTAGAWA, TAKASHI
YAMADA, HIDEAKI
ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-417-090-25

Query Match 40.3%; Score 493.4; DB 3; Length 747;
Best Local Similarity 79.0%; Pred No. 4.4e-154;
Matches 587; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 331 ATGAAAAACGTGTTCTCGCAGTTGTTTTCGCGCAATGTTCTCTCTCAGGCCCTCGGC 390
DB 1 ATGAAAAGCGTGTAATCGCCCTTTCCTGCGCCTCTTTCAGTTAGCGCCCTTTGCG 60

QY 391 CTGGTCGTACGGCAACGACACTACGACGAAACCGGATCTCTACTACTCTCAGACAGT 450
DB 61 CTGGTTCGCGCGCAATGATGATGCCACCAACCGGCGGATCTCTACTATCTGAAAAATGCC 120

QY 451 GAAGCCATTAAACAGCCTGGCGCTGTTGCCGCCACCAACCGCGGTGGCTCCATTGGCTTT 510
DB 121 CAGGCCATTGACAGCCTGGCGCTGTTGCCACCGCGGAACTGGGACAGCTTGGCTTT 180

QY 511 CTCACGATCGGCCCATGTATGAACAGGCGCCTCTGCGGCAACCGCAACCGGTAAG 570
DB 181 TTAACGATCAGCGCATGTATGAAGAGGCGCTCTGCTGCGCGCCACCGCGCGGCGAG 240

QY 571 CTGGCGGCGAAAGATGCAACCTGAGCAGTGGCGGGGTGGCGAATGTTTCTCGGCGCG 630
DB 241 TTGGCGGCGAAGATGCCACCTGAGCGCGGTGGCGGCGCAAGCGCTTCTCGGCGAG 300

QY 631 TTTGGTAGCCGATACCGGAAAGACGCCCCGGCGCTGCAATTAATTAATGACCAATATG 690
DB 301 TTGCGTCCCGGATCAGCGAAAGACGCCCCGGCGCTGCAAACTGCTCACCAATG 360

QY 691 ATTGAGGACGCGGGGATCTGGCGACCGCGAGCGGAAAGATCACTATATGCGCATTCGT 750
DB 361 ATTGAAGACGCGGGCGATCTGGCGACCGCGAGCGGAAAGATATATGCGTATTCGT 420

QY 751 CCGTTTCGCTTTTATGGGCTCTCTACCTGTAAATACCGAGCGGACAACTCTTCCAAA 810
DB 421 CCGTTTGCCTTCTAAGCGGCTGTCACCTGCAATACCAACCGACAGGATAAGCTTCGAAA 480

QY 811 AATGGCTCTTATCCGTCGGGCAATCTCTATCGGCTGGGCTACTCGCTGCTGCGCA 870
DB 481 AAGGCTCTTACCTTCCGACACACCTCTATCGGCTGGGCGACCGCCCTGCTGCGCC 540

QY 871 GAGATCAACCTCAGCGCCAGAACGAGATCTTGAACCGGCTTATGAGCTGGGCGCAGAC 930
DB 541 GAAATCAACCCGACGCGCGAGATGAGATTTCTCAGCGGCTATGAGCTCGGTGAAAGT 600

QY 931 CGGCTGATTTTCGGCTACCACTGSCACAGTGATGATGCGCGCGGCTAGTGGGATCT 990
DB 601 CGGCTGATCTGCGTTTACCACTGSCACAGTGATGATGCGCGCGGCTAGTGGGCTCG 660

QY 991 GCCGTTGGGACCCCTGCATACCAACCGCGGCTTCCAGCAGCAGCTTCCAGAAAGCGAAG 1050
DB 661 GCGGTGTTGCAACCTGSCATACCAATCCGCGCTTCCAGCAGCAGCTGCAAAAGCCAAA 720

1051 GCGGAATTCGCCAGCATCAGAA 1073
721 GACGAGTTTGGGAAACAGCAGAA 743

RESULT 13
US-09-727-578-25
Sequence 25, Application US/09727578
Patent No. 635472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
UTAGAWA, TAKASHI
YAMADA, HIDEAKI
ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
US-09-727-578-25

Query Match 40.3%; Score 493.4; DB 4; Length 747;
Best Local Similarity 79.0%; Pred. No. 4.4e-154;
Matches 587; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

331 ATGAAAACGCTGCTGCGAGTTGTTTGGCGCATGTTCTCTCTCAGGCCCTCGCG 390
1 ATGAAAAGCGTGACTCGCCCTTGCTTGGCTTCCAGCCCTCTTTCAGTTAGCGCCCTTGG 60
391 CTGCTGCGTACCGGCAACGACACTACCGAAGACCGGATCTCTACTACTCAAGAACAGT 450
61 CTGTTCCGCGCGCAATGATGCCACCGACCGCCGATCTCTACTATCTGAAAAATGCC 120
451 GAAGCATTAAAGCCTGCGCTGTGCGGCGACACCGCGGCGTGGCTCCATTCGGTTT 510
121 CAGGCCATTGACGCGCTGCTGTGCCACCGCGCGCGGAGTGGCGAGCATTCGGTTT 180
511 CTCACGATCAGCGCATGTATGAACAGGCGCGCTGTGCGCAACACCGAAGCGGTAAG 570
181 TTAACGATCAGCGCATGTATGAAGAGGCGCTGTGCTGCGCGCACCGCGCGGCAAG 240
571 CTGCGCGCGGAGATGCAAACTGACGAGTGTGCGGGGTGGCGAATGCTTTCTCGGCGCG 630
241 TTGGCGCGCAGAGATGCCAATCTGAGCGCGGTGGCGTGGCGCAAGCCCTTCTCGCGAGCA 300
631 TTGTGATCGGATCACTGAAAAGACCGCGCGCGCTGCAATAATTACTGACCAATG 690
301 TTGCGCTCCCGATCAGCGAAAAGACCGCGCGCGCTGCAAACTGCTCCCAACATG 360
691 ATTGAGGACCGCGGATCTGCGCACCGCGCGCGGAGAAAGATCACTATATGCGCAATCGT 750
361 ATTGAAGACCGGGGATCTGCGACCGCGCGCGGAGGAGAGTATATGCGTATTCGT 420
751 CGGTTTGGGTTTATGGGTCTCTACCTGTATATACCAACCGAGAGCAAACTGTCCAAA 810
421 CGGTTTGGCTTCTACGGCGTGTCCACTGCAATACCAACGAGGATAAGCTGTGAAA 480
811 AATGGCTCTATTCGTCGGGATACCTCTATCGGCTGGGCTACTGCGTGGTGTGGCA 870
481 AACGGCTCTTACCTTTCGGGACACACTCTATCGGCTGGGCGACCGCCCTGGTGGCC 540
871 GAGTCAACCTCAGCGCGCAGACGAGATCTTGAACGCGGTTATGAGCTGGGCCAGAGC 930
541 GAATCAACCGCGCGCAGATGAGTCTTCAACGCGGCTATGAGCTCGTGAAGT 600
931 CGGGTGAATTTGGGCTTACCACTGCGAGAGTGTGGATGCCCGCGGGTGTGGATCT 990

601 CGGGTGAATCTCGGTTTACCATGCGAGCGCATGTTGACGCGCGCGGATGTTGCGCTCG 660
991 GCCGTTGTGGCGACCTGTCATACCAACCGCGCGGTTTCCAGACGAGATTCAGAAAAGCGAAG 1050
661 CGGGTGTGCAACCTGTCATACCAATCCGCGCTTCCAGACGAGCTGCAAAAAGCCAAA 720
1051 GCCGAATTCGCCAGCATCAGAA 1073
721 GACGAGTTTGGAAAACAGCAGAA 743

RESULT 14
US-08-750-145A-2
Sequence 2, Application US/08750145A
Patent No. 6010951
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
TITLE OF INVENTION: Phosphate Ester
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Morganella morganii
STRAIN: NCIMB 10466
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..50
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 61..747

US-08-750-145A-2

Query Match
Best Local Similarity 34.4%; Score 422; DB 3; Length 750;
Matches 545; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 331 ATGAAAACGTTCTGCGAGTTGTTTGGCGGATGTTCTCTCAGGCGCTGGCG 390

DB 1 ATGAAAGAAATTAATGCGCGTGTCTGTTCTGCTACTGTTTCCCTTCCGCGCTGGCC 60

QY 391 CTGGTCGTCACCGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACAGT 450

DB 61 GCGATCCGCGGCGCAACGATGCCACCAAGCGGATTATATATCTGAAAAATGAA 120

QY 451 GAAGCCATTAAACGCTGGCGCTCTTGGCGGACACACCGCGGTGGTCCATTCGGTTT 510

DB 121 CAGGCTATCGACAGCTGAAACTCTTACCGCCACCGCGGAGTGGCGAGTATTCAGTTT 180

QY 511 CTCACGATCAGGCGCATCTATGAACAGGCGGCGCTGCTGCGCAACACCGAACCGCGTAAG 570

DB 181 TTAAATGATCAGGCAATGATGAGAAAGGCGGCTGTGCTGCGCATACCGAGCGCGGAAA 240

QY 571 CTGGCGCGGAAGATGCAAACTTGAGCAGTGGCGGGTGGCGAATGCTTTCTCGCGCGCG 630

DB 241 CAGGACAGGAGATGCTGACCTTGGCGGAGGGGTGTGGCAACCGCATTTTCAGGGGCA 300

QY 631 TTGCTAGCCGATCACCGAAAAAGACGCCCCGGCGCTGCATAAATTAATTAATCAATATG 690

DB 301 TTGCGTATCCGATAACCGAAAAAGACTCTCGCGAGCTGTATAAATCTGCTGACCAATATG 360

QY 691 ATTGAGGACCGCGGGATCTCGCGACCGCGGAGGAGTCTATATATGCGCATTCCT 750

US-08-975-698A-2

Query Match 34.4%; Score 422; DB 3; Length 750;
Best Local Similarity 72.7%; Pred. No. 2.8e-130;
Matches 545; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 331 ATGAAAACGTTCTGCGAGTTGTTTGGCGGATGTTCTCTCAGGCGCTGGCG 390

DB 1 ATGAAAGAAATTAATGCGCGTGTCTGTTCTGCTACTGTTTCCCTTCCGCGCTGGCC 60

QY 391 CTGGTCGTCACCGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACAGT 450

DB 61 GCGATCCGCGGCGCAACGATGCCACCAAGCGGATTATATATCTGAAAAATGAA 120

QY 451 GAAGCCATTAAACGCTGGCGCTCTTGGCGGACACACCGCGGTGGTCCATTCGGTTT 510

DB 121 CAGGCTATCGACAGCTGAAACTCTTACCGCCACCGCGGAGTGGCGAGTATTCAGTTT 180

QY 511 CTCACGATCAGGCGCATCTATGAACAGGCGGCGCTGCTGCGCAACACCGAACCGCGTAAG 570

DB 181 TTAAATGATCAGGCAATGATGAGAAAGGCGGCTGTGCTGCGCATACCGAGCGCGGAAA 240

QY 571 CTGGCGCGGAAGATGCAAACTTGAGCAGTGGCGGGTGGCGAATGCTTTCTCGCGCGCG 630

DB 241 CAGGACAGGAGATGCTGACCTTGGCGGAGGGGTGTGGCAACCGCATTTTCAGGGGCA 300

QY 631 TTGCTAGCCGATCACCGAAAAAGACGCCCCGGCGCTGCATAAATTAATTAATCAATATG 690

DB 301 TTGCGTATCCGATAACCGAAAAAGACTCTCGCGAGCTGTATAAATCTGCTGACCAATATG 360

QY 691 ATTGAGGACCGCGGGATCTCGCGACCGCGGAGGAGTCTATATATGCGCATTCCT 750

RESULT 15

US-08-975-698A-2

Sequence 2, Application US/08975698A

Patent No. 6015697

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO

APPLICANT: UTAGAWA, TAKASHI

APPLICANT: YAMADA, HIDEAKI

APPLICANT: ASANO, YASUHIKA

TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE

TITLE OF INVENTION: ESTER

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SP-VAK, MCCLELLAND, MAIER & NEUSTADT, P. C.

Mon Jun 7 11:07:30 2004

Db	361	ATTGAGGATGCGCGTGATCTTGGCCACCGCTCGGCCAAAGAACATTACATGCGCATCGG	420
Qy	751	CCGTTTCGGGTTTATGGGCTCTACCTGTAATACCACCGAGCAGACAAATGTGTCCAAA	810
Db	421	CCGTTTCGGTTTACGSCACAGAAACCTGTAATACCAAAAGTACAGAAAACATCTCCACC	480
Qy	811	AATGGCTCTTATCCGTCGCGGAGTACTCTATCGGCTGGGCTACTCGCTGTGTCTGGCA	870
Db	481	AACGGATCTTACCGGTGAGGTCTATGCTTATCGGCTGGCAACCGCATGTGTCTGGCG	540
Qy	871	GAGATCAACCTCAGCGCCAGAAACGAGATCCTGAAACGGCGTTATCAGCTGGGCCAGAGC	930
Db	541	GAAGTGAACCGCGCAATCAGAGTGCATCTCGAACGGGTTATCAGCTCGSACAGAGC	600
Qy	931	CGSGTCGATTTGCGGCTACCACTCGCAGAGTGATGTGGATGCCCGCGCGGTAGTGGGATCT	990
Db	601	CGGGTGATTTGCGGCTATCACTGCGAGGTGATGTGGATGCCCGCGCGGATGTGCGGTTCA	660
Qy	991	GCCTTTGTGGCGACCTCGCATACCAACCGCGGCTTCAGCAGCAGTTCAGAAAGCGAG	1050
Db	661	GCOCCTGTGCGCATTTACATTCGGATCCGGCATTTACGGCGGAGTTAGCGAAAGCCAAA	720
Qy	1051	GCAGAAATGCGCCGATCAGAGAAATAA	1080
Db	721	CAGGAATTTGCACAAAATCAGAGAAATAA	750

Search completed: June 4, 2004, 20:42:20
Job time : 92 secs